Hepatitis C virus

OM protein

Run on:

Sequence:

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/note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "N-terminal acetyl"
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/note= "C-terminal amide"
                                           ABB80529
ABB80561
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ABB0536
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    21-JUL-2000; 2000US-220101P.
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Result Š.

Novel human diagno Novel human diagno Hepatitis C virus

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Claim 17; Page 64; 69pp; English.
virus protease
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                                                                                                                                                      pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture a medicament to treat disorders associated with HCV protease. A
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                                                     Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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o. 0.0013; Indels
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                   Brunck TK;
                                                                                         Claim 17; Page 64; 69pp; English
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Best Local Similarity 100.
Matches 11; Conservative
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 (CORV-) CORVAS INT INC
                    Lim-wilby M, Levy OE,
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                                    WPI; 2002-361643/39
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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Length 11;

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a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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al for treating disorders associated with hepatitis C
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DB 23; Let.
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                         /note= "Leucyl carbonyl forming keto-amide linkage with residue 7"
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                                                                          Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.
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tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43.
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ABB80564;

RESULT 7

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                              (CORV-) CORVAS INT INC
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                                             /note= "Norleucyl carbonyl forming keto-amide linkage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide compound having hepatitis C virus protease inhibitory ty useful for treating disorders associated with hepatitis C
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0.0013;
thes 0;
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/note= "N-terminal acetyl"
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                                                                                                                           "C-terminal amide"
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/note= "C-terminal amide'
                                                                        with residue
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                                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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ity useful for treating disorders associated with hepatitis C
        peptide compound having hepatitis C virus protease inhibitory
try useful for treating disorders associated with hepatitis C
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                                                                                                                                                                Length 11;
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/note≈ "C-terminal`amide"
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                                               Claim 17; Page 65; 69pp;
                                                                                                                                                                                     Conservative
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Best Local Similarity
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                             virus protease
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activity
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virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                     Gape
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                                                                                                                                                                                  DB 23;
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Pred. No. 0.00
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100.0%; Pre
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Best Local Similarity 100.
Matches 11; Conservative
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Matches

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"Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
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Pred. No. 0.0088;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                  'note= "N-terminal acetyl"
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                                   ABB80529 standard; peptide; 11 AA.
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90.9%;
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Best Local Similarity 90.90,
Best Local Similarity 10, 500 Servative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
                      Gaрв
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                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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 Pred. No. 0.0088;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brunck TK;
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90.9%;
Similarity 90.9%;
10; Conservative
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                                                                                                                                                                                                                                 (first entry)
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ABB80561;

Best Loc Matches

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                             /note= "Norvaly1 carbony1 forming keto-amide linkage with
residue 7"
                                                   Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide, virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                           Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
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Pred. No. 0.0088;
0; Mismatches 1; Indels
                                                                                                                                                    'note= "N-terminal acetyl"
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                                                                                                                                                                                                                      'note= "D-form residue"
                                                                                                                                                                                                                                                  'note= "Oxymethionine"
                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 65; 69pp; English.
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90.9%;
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(first entry)
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Search completed: December 22, 2003, 17:41:01 Job time : 33.4667 secs

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Sequence 236, App
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                                                                                                                                                                                                                                                December 22, 2003, 16:37:03; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
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: /cgn2 6/ptodata/1/iaa/5A_COMB.pep:*
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: /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-09-328-352-7885
US-08-637-7598-236
US-08-637-7598-236
US-09-201-945-236
US-09-201-945-236
US-09-517197-1
5177197-3
US-08-50-988A-23
US-08-66-66
US-09-521-65-66
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US-08-66-744-4
US-08-460-744-4
US-08-460-777-21
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US-08-463-772-6
US-08-246-361A-4
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 788; Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7885
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OP INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REPREBNCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SEQ ID NO 73
LENGTH: 947
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Sequence 2
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 4; Length 947;
Pred. No. 1.3e+02;
2; Mismatches 1; Indels
                     US-08-464-517-23
US-08-246-361A-6
US-08-246-361A-23
US-08-463-772-23
PCT-US93-0500-23
US-07-4947-10-8
US-08-472-893A-8
US-08-464-517-19
US-08-246-517-20
US-08-246-361A-19
US-08-246-361A-19
US-08-246-361A-20
US-08-463-772-19
US-08-463-772-19
US-08-463-772-19
US-08-463-772-19
US-08-463-772-19
US-08-463-772-19
US-08-463-772-19
US-08-463-772-19
US-08-460-748-2
                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                            Sequence 73, Application US/09228986 Patent No. 6359198 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT

ORGANISM: Pinus radiata
US-09-228-986-73
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686 VMPSGISYS 694
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Best Local Similarity
Matches 6; Conserv
 US-09-328-352-7885
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Score 33; DB 3; Length 45;
Pred. No. 6.6;
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US-09-201-945-236

i Sequence 216, Application US/09201945

i Patent No. 634215

i GENERAL INFORMATION:

APPLICANT: David William Holden

TITLE OP INTENTION: Identification of Genes

NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:

ADDRESSE: Patrea L. Pabst

STREET: 1201 West Peachtree Street

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZITH : 30309-3450

COMPUTER: Floppy disk

COMPUTER: Patentin Release #1.0, Version #1.30

CURRATING SYSTEM: DC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CLASSIPICATION NUMBER: US/09/201,945

FILING DATE:

CLASSIPICATION.
                                                                   CUMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: 31,284
REPERRENEY POCKET INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCY DOCKET NUMBER: 31,284
TELEFONMUNICATION INFORMATION:
TELEFONE (404) 873-8794
TELEFONE CHARACTERISTICS:
LENGURNCE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.5%;
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 REVVPXGMSY 10
                                    Georgia
Atlanta
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Pred. No. 6.6;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Atlanta
STATE: Georgia
CONDITY: USA

ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
RICH APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PADEL, PATE AL.
REGISTRATION: NUMBER: 31,284
REPERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION NUMBER: RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-871-355A-236

Sequence 236, Application US/08871355A

Patent No. 6015669

GENERAL INFORMATION:

APPLICANT: David William Holden

TITLE OF INVENTION: Identification of Genes

NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:

ADDRESSER: Patrea L. Pabat

STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street
                                                                                                                                                                              RESULT 3
US-08-637-759B-236
US-08-637-759B-236
Sequence 236, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.5%;
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EEVVPXGMSY 10
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596 EVVPEGLSF 604
                                    2 EVVPXGMSY 10
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Sequence 66, Application US/09357952

Sequence 66, Application US/09357952

Sequence 66, Application US/09357952

Setent No. 6246904

GENERAL INFORMATION:

APPLICANT: Zhang, Han-Zhong

APPLICANT: Cai, Sui Xiong

APPLICANT: Drewe, John A.

APPLICANT: Wang, Wu

ITILE OF INVENTION: Pluorescence Screening Assays for Caspases, Proteas:

ITILE OF INVENTION: Other Enaymes and the Use Thereof

FILE REFERENCE: 1735.0030001

CURRENT APPLICATION NUMBER: US/09/357,952

CURRENT PILING DATE: 1999-07-21

SEALIER PLING DATE: 21-UL-1998

NUMBER OF SEQ ID NOS: 139

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:Synthetic POTHER INFORMATION: Peptide US-09-357-952-66
                                              S177197-30
; Patent No. 5177197
; APPLICANT: RANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
; APPLICANT: RANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
; MENASTEDT, CHRISTER; HELLMAN, ULP; MIYAZONO, KOHEI; CLAESSON-WELSH,
; LENA; HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMBR OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                Length 1394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 3; Length 10;
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
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                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 6; I
Pred. No. 3.3e+02;
3; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%;
                                                                                                                                                                                                                                                                                                                                                  63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 KBICPGGMGYT 409
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                                    RESULT 8
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                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
517197-51
FACENT NO. 517197
APPLICANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;
HERDIT, CHRISTER;HELLMAN, ULP;MIYAZONO, KOHEI;CLAESSON-WELSH,
LENA;HELDIN, CARL-HENRIK
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING;
HUMAN TRANSFORMING GROWITH FACTOR-BETA1-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
PILING DATE: 27-FEB-1990
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PATENT NO. 5177197

PAPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;

WENNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH,

LENA, HELDIN, CARL-HENRIK

TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING

HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN

NUMBER OF SEQUENCES: 53

CURRENT APPLICATION DATA;

PILING DATE: 27-PEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 410;
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Pred. No. 10;
                                                                                                                                                                                                                                                                                                             Score 33; DB 4; Length 45; Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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Pred. No. 81;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                      RPMS 101
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEPAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%;
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Best Local Similarity 45.5
Best Local Similarity 45.5
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 45.5
Matches 5, Conservative
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399 KEICPGGMGYT 409
                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGMSYS 11
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52 KEICPGGMGYT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                   ||: | | ||
1 ERISPLGWSY 10
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5177197-1
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Gaps

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| Sequence 23, Application US/08580988A
| Patent No. 5856161
| GENERAL INFORMATION:
| APPLICANT: Aggarwal et al.
| TITLE OF INVENTION: Tumor Necrosis Factor
| TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
| TITLE OF INVENTION: For Its Use
| NUMBER OF SEQUENCES: 27
| CORRESPONDENCE ADDRESS:
| ADDRESSER: Dr. Benjamin A. Adler
| STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.5%; Score 32; DB 2; Length 102; 60.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ABDESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELECHONE: 713-777-6908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 1.44 Mb floppy disk COMFUTER: Apple Macintosh OPERATING SYSTEM: Macintosh SOFTWARE: Microsoft Word for Macintosh ADDIICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/580,988A FILING DATE: January 3, 1996 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INPORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 102 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEVVPXGMSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: no
PRAGMENT TYPE: i
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                          US-08-580-988A-23
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US-08-460-694-4
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Fater No. 6342611
GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cai, Sui Xiong
APPLICANT: Cana, John A.
TITLE OF INVENTION: No. 6342611e1 Fluorogenic or Fluorescence
TITLE OF INVENTION: No. 6342611e1 Fluorogenic or Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
TITLE OF INVENTION: Use Thereof
TITLE OF USE THE STORM UNBER: US 60/61,582
EARLIER FILING DATE: 1999-10-09
EARLIER FILING DATE: 1999-10-09
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE FILING USE: USE OF USE O
                TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescence TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the FILE REFERENCE: 1735.029002
CURRENT APPLICATION WUMBER: US/09/521,650
CURRENT APPLICATION NUMBER: 09/168,888
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER FILING DATE: 1998-10-09
EARLIER PILING DATE: 1997-10-10
EARLIER PILING DATE: 1997-10-10
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 1.9; 2; Indels ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.5%; Score 32; DB 4; Length 10; 50.0%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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ORGANISM: Artificial Sequence
APPLICANT: Zhang, Han-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DDIVPCSMSY 10
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Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-521-650-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 66
LENGTH: 10
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LENGTH: 10
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Gapa ö

Indels

Gapa

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Score 32; DB 3; Length 152;
Pred. No. 42;
1; Mismatches 3; Indels
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Pred. No. 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ARROLD, ANDREW
TITLE OF INVENTION: Pradi Cyclin and Its cDNA
INDRER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: STERRE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/07/667,711B
FILING DATE: 11-MAR-1991
CLASSIFICATION NOWBER: US/07/667,711B
FILING DATE: 11-MAR-1991
CLASSIFICATION NOWBER: 35
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35
TELEPOMMICATION INFORMATION:
TELEPOMMICATION INFORMATION:
TELEPOMMICATION INFORMATION:
TELEPOMMICATION OF SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
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US-07-667-711B-4
; Sequence 4, Application US/07667711B
; Patent No. 610700
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60.0%;
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60.0%;
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TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: peptide
US-07-667-711B-4
                                                                                                                                     Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6, Conservative
             p TOPOLOGY: linear
p MOLECULE TYPE: peptide
US-08-460-744-4
                                                                                                                                                                                                                                                             1 EEVVPXGMSY 10
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15 Sequence 4, Application US/08460744

1 Sequence 8, Application US/08460744

1 Patent No. 6107541

2 GENERAL INFORMATION:
ATITLE OF INVENTION: PRADI Cyclin and its CDNA
TITLE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES:
COUNTESPONDENCE ADDRESSS:
ADDRESSEE: STRENB, ECX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
STATE: DC
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: 120005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 2; Length 152;
Pred. No. 42;
1; Mismatches 3; Indels
                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: RIODSY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATENTIAN PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLLASSIFICATION: 425
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 0609.4070002
TELEFRAM: 202-371.2600
TELEFAX: 202-371.2600
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCONCATNY, EVELYN H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET UNBER: 35,279
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative :
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-08-460-694-4
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DC
USA
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December 22, 2003, 16:40:14 ; Search time 20.8667 Seconds (without alignments) 98.451 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                696363 segs, 186758610 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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52
1 EEVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 4, Appli		4	4	324	Sequence 32076, A	Sequence 2565, Ap		Sequence 4, Appli	Sequence 67, Appl	Sequence 2, Appli	Sequence 7477, Ap	Sequence 43, Appl	Sequence 108, App	Semience 108. App
	ΩI	US-10-029-120-4	US-10-027-806-4	US-10-034-623-4	US-10-027-801-4	US-10-029-386-32486	US-10-029-386-32076	US-10-094-749-2565	US-10-101-464A-73	US-10-122-067-4	US-10-096-534-67	US-10-122-067-2	US-10-106-698-7477	US-10-214-766-43	US-09-992-600A-108	US-09-924-340-108
		12	14	14			12		15		12			15		
	Query Match Length DB	3472	3472	3472	3472	153	236	290	947	1163	1499	1499	66	426	478	478
æ	Query Match	73.1	73.1	73.1	73.1	69.2	67.3	65.4	65.4	65.4	65.4	65.4	63.5	63.5	63.5	63.5
	Score	38	38	38	38	36	35	34	34	34	34	34	33	33	33	33
	Result No.			, 3	4	ß	9	7	σ	σ	10	11	12	13	14	15

Sequence 184, App Sequence 108, App Sequence 108, App Sequence 108, App Sequence 108, App	108, 3010, 26, A 130, 261,	sequence 66, Appl Sequence 241, Appl Sequence 2076, Ap Sequence 53, Appl Sequence 53, Appl	24, A 4, A 275, 1061	Sequence 2, Appli Sequence 4, Appli Sequence 10384, A Sequence 467, App Sequence 4, Appli Sequence 878, App Sequence 878, App Sequence 878, App
11 US-09-746-783-184 12 US-09-992-095B-108 12 US-10-154-678-108 12 US-09-999-570-108 15 US-10-000-489-108	15 US-10-000-986-108 12 US-10-094-749-3010 11 US-09-823-136 16 US-10-080-170-130 17 US-10-116-275-261	12 US-10-138-375-66 12 US-10-139-375-66 12 US-10-199-820-241 12 US-10-094-749-2076 12 US-0-778-927A-53 12 US-10-116-275-114	Þ	9 US-09-925-731-2 15 US-10-101-921-4 9 US-09-815-242-10384 12 US-10-287-274-467 14 US-10-151-736-4 16 US-09-764-878 15 US-10-092-154-878 16 US-09-948-080-14
478 478 478 478	478 648 653 1152 1394	245 254 254 254 254 254 254 254	0 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	691 1377 1377 2799 53 53
63.5 63.5 63.5 63.5	0.000 0.000 0.000 0.000 0.000	61.5 61.5 61.5 61.5	61.5 61.5 61.5 61.5	61.5 611.5 611.5 611.5 59.6 59.6
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16 117 119 20	4 64 64 64 64 64 64 64 64 64 64 64 64 64	9 9 9 8 7 6 1 0 9 8 7 6	BBBBBB BBBBB BBBBB	8 6 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

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Sequence 4, Application US/10029120
; Sequence 4, Application US/10029120
; Publication No. US20030175708A1
; GRENEAL INFORMATION:
    APPLICANT: Swanson, Rohart A.
    APPLICANT: Swanson, Rohart A.
    APPLICANT: Shelper. Christa
    ITILE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
    FILE REFERENCE: DOORP.002A
    CURRENT PILING DATE: 2001-12.1
    PRIOR APPLICATION NUMBER: US/10/029,120
    CURRENT PILING DATE: 2001-12.2
    PRIOR PILING DATE: BARLIER FILING DATE: 1999-09-29
    NUMBER OF SEQ ID NOS: 123
    SOFTWARE: PARESEQ for Windows Version 3.0
    FERGING A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10027806; Publication No. US20020160476A1; GENERAL INFORMATION: APPLICANT: Swanson, Robert A.; APPLICANT: Feldman, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2294 EDVIPRGISFS 2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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Best Local Similarity
Matches 6; Conserv
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US-10-029-120-4
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LENGTH: 3472
    SEQ ID NO 4
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APPLICANT: Seanson, Robert A.
APPLICANT: Scaleper, Christa
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT PELING NUMBER: US/10/034,623
CURRENT FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10027801
Publication No. US20030054364A1
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
ATTILE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT PILING DATE: 2001-12-1
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
APPLICANT: Schleper, Christa
TITLE OF INTENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.0025
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21
PRIOR PILING DATE: EARLIER PILING DATE: 1999-09-29
SOFTWARE: RABLIER FILING DATE: 1999-09-29
SOFTWARE: PARTIES FOR WINDOWS VERSION 3.0
SEQ ID NOS: 123
SOFTWARE: PARTIES FOR WINDOWS VERSION 3.0
ENGTH. 3472
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Pred. No. 1.6e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 14; Length 3472;
Pred. No. 1.6e+02;
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Publication No. US20020198365A1
GENERAL INFORMATION:
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ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                               TYPE: PRT ; ORGANISM: Cenarchaeum symbiosum US-10-027-806-4
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 54.5%;
Matches 6; Conservative
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2294 EDVIPRGISFS 2304
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US-10-027-801-4
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Sequence 32466, Application US/10029386

Sequence 32466, Application US/10029386

Sequence 32466, Application US/20030194704A1

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: HARAN, David R.
APPLICANT: HARAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL POR FILE OF INVENTION: BENERGESION ANALYSIS TWO FILE OF INVENTION: NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 32486

LENGTH A.
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: BANDESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS
TOTAL OF THE ANALYSIS TO NOS: 34288
SOFTWARR: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32076
LENGTH: 236
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                                                                                                              Score 38; DB 15; Length 3472;
Pred. No. 1.6e+02;
4; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO AF002994.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: WISSPROT HIT: P43363, EVALUE 5.00e-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 32076, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
TYPE: PRT; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-4
                                                                                                                    73.1%;
54.5%;
                                                                                                                                                                                                                                                                     |:|:| |:|:|
2294 EDVIPRGISFS 2304
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                 Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                      1 BEVVPXGMSYS 11
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ORGANISM: Homo sapiens
PEATURE:
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APPLICANT: Strabala, Timothy
APPLICANT: Mieuwenhuizen, Nicolaas
APPLICANT: Mieuwenhuizen, Nicolaas
APPLICANT: Mieuwenhuizen, Nicolaas
APPLICANT: Mieuwenhuizen, Nicolaas
APPLICANT: Mieuwenhuizen, Nicolaen M.
TITLE OF INVENTION: Conjocations Isolated from Plant Cells
TITLE OF INVENTION: Conjocations Isolated from Plant Cell Signaling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
CURRENT FILING DATE: 2002-03-18
FRIOR APPLICATION NUMBER: 09/704,302
FRIOR PLILING DATE: 1999-01-01
FRIOR PLILING DATE: 1999-11-01
FRIOR PLILING DATE: 1999-11-01
FRIOR PLILING DATE: 2000-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 67, Application US/10096534
Publication No. US20030166887A1
GENERAL INFORMATION:
APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Yates, Karen
APPLICANT: Missuno, Shuichi
APPLICANT: Missuno, Shuichi
APPLICANT: Glowacki, Julie
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SKELETAL DEGENERATION CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.4%; Score 34; DB 15; Length 947; 66.7%; Pred. No. 2.5e+02;
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Publication No. US20030165883A1
GENERAL INPORMATION:
TITLE OF INVENTION: 27091, A PHOSPHOLIPID TRANSPORTING
TITLE OF INVENTION: ATPASE MOLECULE AND USES THEREFOR
TITLE OF INVENTION: ATPASE MOLECULE AND USES THEREFOR
TILE REFERENCE: WID10.058PIR
CURRENT APPLICATION NUMBER: US/10/12,067
CURRENT PLING DATE: 2002-04-12
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FARLSEQ for Windows Version 4.0;
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Pinus radiata
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686 VMPSGISYS 694
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ORGANISM: Homo sapiens
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Best Local Similarity
Them 8; Conserve
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                                                                                                                                                                                                                                                                                            Score 35; DB 12; Length 236;
Pred. No. 32;
2; Mismatches 1; Indels
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; OTHER INFORMATION: MAP TO 298050.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3
US-10-029-386-32076
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REPERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR PELLOATION NUMBER: 60/350,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN Ver. 2.1
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US-10-101-464A-73
; Sequence 73, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: MAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HOO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAGAI, KEIICHI
IRIB, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                 67.3%;
                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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EEIVPMGIS 43
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Best Local Similarity
Matches 6; Conserv
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Matches 6: Conserv
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LENGTH: 290
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APPLICANT:
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                                                             OTHER INFORMATION: (57)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (58)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE

    i LOCATION: (93)
    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-7477

                                                                                                                                                                             LOCATION: (14) -
OTHER INPORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FRATURE
                                                                                                                                                                                                                                    LOCATION: (39)—
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                LOCATION: (40) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC_FEATURE
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Sequence 43, Application US/10214766

Sequence 43, Application No. US2030084473A1

GENERAL INPORMATION:

APPLICANT: Gocal, Greg

TITLS OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS

FILE REFERENCE: CA1138

CURRENT APPLICATION NUMBER: US/10/214,766

CURRENT APPLICATION NUMBER: US 60/311,734

PRIOR APPLICATION NUMBER: US 60/311,734

PRIOR PILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 53

SOFTWARE PALENT VERSION 3.2

SEQ ID NO 43

LENGTH: 426
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Pred. No. 1.6e+02;
1; Mismatches 3; Indels
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; Pred. No. 32;
2; Mismatches 1; Indels
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60.0%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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ORGANISM: Vibrio cholerae
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                                                                                                                                                             NAMB/KBY: MISC_PEATURE
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73 LVPVGISYS 81
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Publication No. US20030109690A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR APPLICATION NUMBER: PCS 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
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Pred. No. 4.2e+02;
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Pred. No. 4.2e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                    3; Indels
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Publication No. US20030165883A1
GENERAL INFORMATION:
APPLICANT. ROLY AJ. CURTIS
TITLE OF INVENTION: 27091, A PHOSPHOLIPID TRANSPORTING
TITLE OF INVENTION: ATPASE MOLECULE AND USES THEREFOR
FILE REFERENCE: MP101-05891R
CURRENT APPLICATION NUMBER: US/10/122,067
CURRENT FILING DATE: 2002-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                    0; Mismatches
FILE REFERENCE: B0801/7244/KA/ERP
CURRENT APPLICATION NUMBER: US/10/096,534
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US 60/274,980
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.0
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Best Local Similarity 72...
8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-096-534-67
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US-10-122-067-2
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LENGTH: 1499
TYPE: PRT
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LENGTH: 99
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US-09-924-340-108

Sequence 108, Application US/09924340

Publication No. US20030027248A1

GENERAL INFORMATION:

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.US2.REG

CURRENT PILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/299,698

PRIOR APPLICATION NUMBER: US 60/299,574

PRIOR PLING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 112

SOFTWARE: JPAtent

SEQ ID NO 108

LENGTH: 478

LENGTH: 478
                                                                                       APPLICANT: Benatalous:
APPLICANT: Benatalous:
APPLICANT: Tanaka, Hiroaki
FILE OF INVENTION: HUMAN CONAS AND PROTEINS AND USES THEREOF
FILE REPERENCE: 91.U54, DIV
CURRENT FILING DATE: 2001-11-13
FRIOR PELICATION NUMBER: US 09/924,340
PRIOR PLICATION NUMBER: PCT/IB01/01715
PRIOR PELING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PLICATION NUMBER: US 60/305,456
PRIOR PLICATION NUMBER: US 60/305,456
PRIOR PLICATION NUMBER: US 60/302,277
PRIOR PLICATION NUMBER: US 60/302,277
PRIOR PLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-29
PRIOR PLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 114
SOFTWARE: JBatent
SEQ ID NO 108
LENGTH: 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.5%; Score 33; DB 11; Length 478; Best Local Similarity 60.0%; Pred. No. 1.9e+02; Matches 6; Conservative 1; Mismatches 3; Indels
                        Sequence 108, Application US/09992600A Publication No. US20030027161A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-600A-108
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; ORGANISM: Homo sapiens
US-09-924-340-108
US-09-992-600A-108
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Qy 2 EVVPXGMSYS 11
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Db 239 EVAPAGASYN 248
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Search completed: December 22, 2003, 17:32:42 Job time : 20.9333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 22, 2003, 17:24:36; Search time 9.06667 Seconds (without alignments) 116.675 Million cell updates/sec Run on:

US-09-909-164-10 52 1 BEVVPXGMSYS 11

Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical 367K	probable sulfate p	sulfate permease -	V1 protein - tobac	DNA segregation AT			zinc finger protei	topoisomerase IV s	DNA-binding protei	hypothetical prote			hypothetical prote	_	hypothetical prote			hypothetical prote	~	hypothetical prote		cdc37 protein - fi	iron(III) ABC tran	bacteriocin BCN5 -	ATP-dependent DNA	conserved hypothet	transforming growt	DNA-directed RNA p
SUMMARIES	ID	T31308	T39116	T40413	A42452	B97355	S57810	T24111	S22293	H82691	A34203	S54619	H69491	C82900	140758	E90544	D69493	C81374	T34536	875817	T47670	F72281	D82163	T43653	D82352	A30481	AF3286	D87046	A35626	G82336
	DB	7	~	~	~	7	N	N			~			N	~	~	N	7									N	~	~	7
	* Query Match Length	3472	840	877	102	1498	225	425	670	749	2717	156	252	544	94	116	165	253	259	284	298	368	426	466	653	890	1028	1152	1394	1401
	& Query Match	73.1	71.2	71.2	69.2	69.2	67.3	67.3	67.3	67.3	67.3	65.4	65.4	n	ന	63.5	63.5	63.5	63.5	•	63.5	٠	63.5	63.5	63.5	•	63.5	٠	•	63.5
	Score	38	37	37	36	36	35	35	32	35	35	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
	Result No.		7	m	4	ß	9	7	89	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

hypothetical prote masking protein pr	transport protein rho protein GDP-di hypothetical prote cyclin D2 - rat	cyclin D2 - rat cyclin D2 - mouse cyclin D2 - human cyclin D1 - Africa	cyclin D2 - Africa cyclin D2 - chicke cyclin D1 - zebra cyclin D3 - human cyclin D1 - human
T04456 A38261 B97333	P00616 T01457 B72481 JC4011	IS8372 A41984 A42822 S57922	S57925 JC4579 S62730 B42822 A38977
000	0000	0000	00000
1548 1712 84	175 223 279 288	288 289 291	291 291 292 295
63.5 63.5 61.5	61.5 61.5 61.5	61.5 61.5 61.5	61.5 61.5 61.5 61.5
8 8 8 8 8 8 8 8 8	3555	2222	88888 8888
30 31 32	6 6 6 6 6 4 6 6	33 38 40 40	4 4 4 4 4 11 52 52 4 73

# ALIGNMENTS

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hypothetical 367K protein - Cenarchaeum symbiosum
C;Species: Canarchaeum symbiosum
C;Species: Canarchaeum symbiosum
C;Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T31308
R;Schleper, C.; DeLong, E.F.; Preston, C.M.; Peldman, R.A.; Wu, K.Y.; Swanson, R.V.
J. Bacteriol. 180, 5003-5009, 1998
A;Title: Genomic analysis reveals chromosomal variation in natural populations of the A;Reference number: 220994; MUID:98422450; PMID:9748430
A;Reference number: 220994; MUID:98422450; PMID:9748430
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 13472 cSCH>
A;Residues: L3472 cSCH>
A;Acrose-references: EMBL:AF0833072; NID:93599393; PID:93599394; PIDN:AAC62699.1
C;Superfamily: Cenarchaeum symbiosum hypothetical 367K protein
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ö Gaps ö / Match 73.1%; Score 38; DB 2; Length 3472; Local Similarity 54.5%; Pred. No. 59; loss 6; Conservative 4; Mismatches 1; Indels Query Match Best Local S Matches 6

|:|:| |:||:| 2294 EDVIPRGISFS 2304 1 BEVVPXGMSYS 11 ઠે 셤

probable sulfate permease - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Accession: 139116
B;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, November 1999
A;Rocession: T39116
A;Rocession: T39116
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule : Type: DMA
A;Rolecule : Type: DMA
A;Residues: 1-840 cHUNA
A;Residues: 1-840 cHUNA
A;Residues: BMBL:AL132779; PIDN:CAB60015.1; GSPDB:GN00066; SPDB:SPAC869.05c
A;Experimental source: strain 972h-; cosmid c869

C;Genetics: A;Gene: SPDB:SPAC869.05c

A; Map position: 1

Gapa ; 0 Query Match 71.2%; Score 37; DB 2; Length 840; Best Local Similarity 77.8%; Pred. No. 21; Matches 7; Conservative 1; Mismatches 1; Indels

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||| ||||: 135 VVPQGMSYA 143 3 VVPXGMSYS 11

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withited to the EMBL Data Library, October 1996
A; Reference number: 219842
A; Reference number: 219842
A; Reference number: 219842
A; Accession: T2111
A; Status: pre-liminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-425
A; Residues: 1-425
A; Residues: 1-425
A; Cross-references: EMBL: 281109; PIDN: CAB03241.1; GSPDB: GN00023; CESP: R10D12.10
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zinc finger protein AT-BP2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C;Accession: $22233 i78658
R;Mitchelmore, C.; Traboni, C.; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C'Species: Caenorhabditis elegans
C'Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C'Accession: T24111
R;Percy, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein precursor (clone TPP11) - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cipacesion: S57810

Riwilligan, S.B.; Gasser, C.S.

Plant Mol. Biol. 28, 691-11, 1995

A;rtie: Neture and regulation of pistil-expressed genes in tomato.

A;reference number: S57808; MUID: 95375233; PMID: 7647301

A;Accession: S57810

A;Accession: S57810

A;Accession: S57810

A;Accession: S57810

A;Accession: S57810

A;Reference: RMNA

A;Residues: 1-225

A;Cross-references: RMBL: U20592; NID: 9924625; PIDN: AAA80497.1; PID: 9924626

C;Superfamily: plant Kunitz-type proteinase inhibitor
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Score 36; DB 2; Length 1498;
Pred. No. 63;
2; Mismatches 2; Indels
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Pred. No. 13;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein R10D12.10 - Caenorhabditis elegans
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        Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                            |: :| ||||
1276 BQKIPMGMSY 1285
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335 RQIVPGGLQY 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A45452
R;Morris, Ba.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.B.
Virology 187, 633-642, 1992
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yello
                                                                                                                                                            Cispecies: Schizosaccharomyces pombe
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
Cibacession: T40419
Silvne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
Submitted to the EMBL Data Library, August 1998
A.Reference number: 221926
A.Accession: T40413
A.Accession: T40414
A.References: EMBL:AL031261; PIDN:CAA20298.1; GSPDB:GN00067; SPDB:SPBC3H7.02
A.Forberimental source: strain 972h-; cosmid c3H7
Cigenetics:
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A,Molacule type: DNA
A,Residues: 1-102 <MOR>
A,Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 22;
1; Mismatches 1; Indels
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60.0%; Pred. No. 3.5;
tive 3; Mismatches 1; Indels
                                                                                                                                - fission yeast (Schizosaccharomyces pombe)
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Best Local Similarity 77.8%;
Matches 7; Conservative 1
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Best Local Similarity 60.0
Matches 6; Conservative
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7 QVVPSGINYS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: SPDB:SPBC3H7.02
A,Map position: 2
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Nypotherical protein YOR013w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein 02612; hypothetical protein YOL303.3
Cispeciaes Saccharomyces cerevisiae
C; Date: 08-301-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C; Accession: S54619; 866879
R; Ade Haan, M.; Maarse, A.C.; Grivell, L.A.
Ryde Hann, M.; Maarse, A.C.; Grivell, L.A.
Ryde Hence number: S54617
A; Reference number: S54617
A; Residues: 1-156 coEH>
A; Residues: 1-156 coEH>
A; Residues: 1-156 coEH>
A; Residues: 1-156 coEH>
A; Reference number: S66877
A; Reference number: S66877
A; Reference number: S66877
A; Reference number: S66879
A; Residues: 1-156 coEM>
A; Reference number: S66877
A; Residues: 1-156 coEM>
A; Residues: 1-150 coEM>
A; Res
                                                                                                           cell division inhibitor (minD-2) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 26-Aug-1999
C;Accession: H69491
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dods; R;Klenk, H.P.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
    A;Title: A DNA-binding protein containing two widely separated zinc finger motifs that A;Reference number: A34203; MUID:90169514; PMID:2106471
A;Accession: A34203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.3%; Score 35; DB 2; Length 2717; 66.7%; Pred. No. 1.9e+02; ive 2; Mismatches 1; Indels
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Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: hypothetical protein YOR013w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.3
Best Local Similarity 66.7
Matches 6; Conservative
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nes 6; Conservative
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2405 WVPAGLTYS 2413
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coposemerase I vacuumit XR1353 (imported) - Xylella fastidiosa (strain 985c)
C;Species: Xylella fastidiosa
C;Species: Mylella 
A;Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-A;Reference number: IS8280; MUID:91187610; PMID:1901405
A;Accession: 822293
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: XP1353
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               topoisomerase IV subunit XF1353 [imported] - Xylella fastidiosa (strain 9a5c)
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                                                                                                                                                     A; Molecule type: mRNA
A;Residues: 1-670 <MIT>
A;Residues: 1-670 <MIT>
A;Cross-references: RMBL:X54250; NID:g57519; PIDN:CAA38151.1; PID:g57520
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 2; Length 670;
Pred. No. 43;
2; Mismatches 1; Indels
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Pred. No. 48;
0; Mismatches
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77.8%;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 VVPAGLTYS 384
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Gaps

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2; Indels

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508 ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: E90544
R;Chambaud, 1.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, P.; Moszer, I
Nucleic Acids Res. 29, 2145-2153, 2001
A;Reference number: A99512; MUID:21267165; PMID:11353084
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Nature 390, 364-370, 1997
Aluthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: H69491
A;Status: preliminary: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-252 cKLE>
A;Residues: 1-252 cKLE>
A;Cross-references: GB;AE000970; GB:AE000782; NID:g2689293; PIDN:AAB89318.1; PID:g264866
C;Superfamily: cell division inhibitor minD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein 1 - Campylobacter jejuni (fragment)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C;Accession: 140758; 447317
J:Bacteriol: 177, 2396-2402, 1995
A;Hani, B.K.; Chan, V.L.
J:Bacteriol: 177, 2396-2402, 1995
A;Title: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd
A;Reference number: 140758; MUID:95247673; PMID:7730270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: C82000 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-544 <GLA>
A;Cross-references: GB:AE002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
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A;Residues: 1-94 <RES>
A;Cross-references: RMBL:Z36940; NID:g535805; PIDN:CAA85392.1; PID:g535806
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Pred. No. 24;
1; Mismatches 1; Indels
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Pred. No. 14;
2; Mismatches 2; Indels
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55;
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Pred. No.
                                                                                                                                                                                                                                                                                                                 65.4%;
ilarity 75.0%;
Conservative
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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26 DIFPSGMSY 34
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81 EVIPAGMS 88
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
6; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                        EVVPXGMS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: C;Genetics: A;Gene: ABCsbp-5; UU359 A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary A;Molecule type: DNA
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A;Molecule type: DNA
A;Reaidues: 1-116 «KUR»
A;Cross-references: GB:AL445566; PID:g14089674; PIDN:CAC13434.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
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                                                                                                                                                                                                      Score 33; DB 2; Length 116;
Pred. No. 17;
0; Mismatches 2; Indels
                                                                                                               A.Gene: MYPU 2610
A.Genetic code: SGC3
C.Superfamily: Bscherichia coli ribosomal protein L20
                                                                                                                                                                                                        Query Match 63.5%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                 3 VVPXGMSYS 11
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 22, 2003, 16:43:51; Search time 4.6 Seconds (without alignments) 112.455 Million cell updates/sec Run on:

US-09-909-164-10 52 1 EEVVPXGMSYS 11 Title: Perfect score: Sequence:

Scoring table:

127863 seqs, 47026705 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTES

		teri	acch	yel	dium	pien	ora	pien	вта	glob	bact	culu	chol	acch	pien	dium	culu	pien	chol	pien	norv	culu	norv	pien	culu	anio	lae	gall	lae	gall	sapien	sapien	musculu	norv
	ption	fusobacteri	schizosacch	tobacco yel	clostridium	homo sapien	neurospora	homo sapien	mycoplasma	archaeoglob	campylobact	mus musculu	vibrio chol	schizosacch	homo sapien	clostridium	mus musculu	homo sapien		homo sapien		mus musculu		homo sapien	mus musculu	brachydanio	xenopus lae	gallus	xenopus lae	gallus gall	homo sa	homo saj	was mus	rattus
	Description	08rq86	074377	P31619	204351	P15822	P23622	060312	098qv0	028330	P45489	Q9d387	Q9krb0	094740	Q9nzm5	P08696	Q8cg18	P22064	09kv29	014766	000018	Q8cg19	004827	P30279	P30280	090459	P50755	P49706	P53782	P55169	P30281	P24385	P25322	P39948
SUMMARIES	0	CARB FUSIN	SULH SCHPO	Y11K_TYDVA	Y1A9_CLOAB	ZEP1_HUMAN	CY14_NEUCR	A10C HUMAN		YJ49 ARCFU	Y990 CAMJE	CTX3 MOUSE	OA_VIBCH	CC37 SCHPO	3R2 HUMAN	NS_CLOPE	LTBS_MOUSE	'BS_HUMAN	RPOC_VIBCH	TBL HUMAN	TB1_RAT	LTBL_MOUSE	3D2 RAT	3D2_HUMAN	SD2 MOUSE	CGD1 BRARE	CGD1_XENLA	CGD2_CHICK		CGD1_CHICK	CGD3_HUMAN	CGD1 HUMAN	CGD1_MOUSE	CGD1_RAT
	DB 1D	5	1 St	1 Y1		1 ZE			1 R	2	7.5		1 AF	2		1 BC	5	5	1 RE		5								r S		8	S	20	 8
	Length D	1058	877	102	1498	2717	788	1499	116	165	253	280	426	466	478	890	1389	1394	1401	1595	1712	1713	288	289	289	291	291	291	291	292	292	295	295	295
J	Query Match	73.1	71.2	69.2	69.5	67.3	65.4	65.4	•	٠				63.5			63.5		63.5	•	•		•		•	•				•	٠	61.5	٠	61.5
	Score	38	37	36	36	35	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32
	Result No.	, 1	7	e	4	ß	9	7	8	Ø	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	29	30	31	32	33

7 haemophilus 5 homo sapien					
P44677 075355	09y61 P9051	P5238	Q6267 P2893	P16916 P16918	P16917 095071
TOLB HABIN	S216 HUMAN GSP CRIPA	PRTP HSV6U SCT1 YEAST	EDD RAT	RHSA ECOLI	RHSB_ECOLI EDD_HUMAN
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427 529	691 719	726	920	1377	1411 2799
N. W.	5. 5.	5	5	61.5	9.50
61	6 6	6 19	61	6.6	61
32	35	35	32	35 2	333
3.5	36	38	<del>2</del> 4	4 4	4 4 5

## ALIGNMENTS

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-1- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY SIMILARITY).
                         genome sequence of Schizosaccharomyces pombe.";
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WEDIANS-21840401; PubMed=11859360;
WEDIANS-21840401; PubMed=11859360;
WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Boquros U., Berown S., Chillingworth T., Churcher C.M., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gollins M., Connor R., Hamlin N., Harris D., Hidalgo U., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huchel E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Murpby L., Niblett D., Odell C., Oliver K., O'Neil S., Mangall K., Murpby L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Antherford K., Rutter S., Sauders R., Squares S., Stevens K., Anylor K., Taylor K., Taylor K., Taylor K., Walsh S.V., Warren T., Whitehead S., Nocdward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Goltwa K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Actions T., Changer E., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S., Malbert P., Dominguez A., Revuelta J.L., Moreno S., Amristrong J., Forsburg S.L., Abnanguez A., Revuelta J.L., Moreno S., Annstrong J., Forsburg S.L., Abnanguez A., Revuelta J.L., Moreno S., Annstrong J., Forsburg S.L., Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
R PIGREAMS, TIGRO1369; CPSASE.
R TIGREAMS, TIGRO1369; CPSASE.
R PROSITE; PRO00866; CPSASE.
R PROSITE; PS00866; CPSASE.
R PROSITE; PS00867; CPSASE.
R Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
KW Arginine biosynthesis; Pyrimidine CARBOXPHOSPHATE SYNTHETIC DOMAIN.
FT DOMAIN 402 546 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
FT DOMAIN 402 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
FT ALLOSTERIC DOMAIN.
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ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

117451 MW; ED7037AF77CIE39F CRC64;
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Pred. No. 6.3;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
Probable sulfate permease C3H7.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              877 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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190 EIVPNGLNYS 199
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208
228
300
832
832
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074377;
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REPEAT
NP BIND
NP BIND
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SULH SCHPO
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SEQUENCE FROM N.A.

MORTIS B.A.B., PubMed=1546458;

MORTIS B.A.B., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

Mortis B.A.B., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

"The nucleotide sequence of the infectious cloned DNA component of

"The nucleotide sequence of the infectious cloned DNA component of

"The nucleotide sequence of the infections of geminiviruses

infecting monocotyledonus plants.";

Virology 187:613-642(1992).
-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
-i- SIMILARITY: Contains 1 STAS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.2%; Score 37; DB 1; Length 877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          594 747 SIAS.
877 AA; 96373 MW; 56995A8493371B43 CRC64;
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Viruses, 88DNA viruses, Geminiviridae, Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YIIK TYDVA STANDARD; PRT; 102 AA. P31619; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last Bequence update) 01-OCT-1993 (Rel. 27, Last annotation update) Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 8.4
1; Mismatches
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                           EMBL; AL031261; CAA20298.1; --
PIR; T40413; T40413.
GeneDB SPenbe; SPR61347.02; --
InterPro; IPR001645; STAS.
InterPro; IPR001902; Sulph_transpt.
Pfam; PP001740; STAS; 1.
Pfam; PP00176; Sulfate transp; 1.
TIGRPAMS; TIGR00815; Sulp; 1.
PROSITE; PS010130; SLC26A; 1.
PROSITE; PS010130; SLC26A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 VVPQGMSYA 156
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NCBI_TaxID=31599;
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PROSITE; PS50901; FTSK\_SPOIIIE; 2.
Hypothetical protein; ĀTP-binding; Complete proteome; Repeat.
DOMAIN 655 857 FTSK/SPOIIE 1.
NP BIND 675 682 ATP (POTENTIAL).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sauer U., Duerre P.;
"Sequence and molecular characterization of a DNA region encoding a small heat shock protein of Clossridium acetobutylicum.";
J. Bacteriol. 175:334-3400(1993).
-!- SIMILARITY: Contains 2 FERK/SpolIIE domains.
-!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINB=21359325; PubMed=11466286;

Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin B.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                Score 36; DB 1; Length 102;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                 102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 28, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1498 AA.
                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-108 FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=93273706; PubMed=8501044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X65276; CAA46379.1; ALT FRAME.
PIR; B97355; B97355.
InterPro; IPRO2543; Ft&K SpoilE.
Pfam; PF01580; Ft&K SpoilE; 2.
                                                                                                                                                                     PIR; A42452; A42452.
InterPro; IPR002631; Gemini mov.
Pfam; PP01708; Gemini_mov; T.
Hypothetical procein.
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                                                                                                                                                                                                                                                                                    69.2%;
                                                                                                                                                    EMBL; M81103; AAA47947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein CAC3709
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                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    OVVPSGINYS 16
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-2003
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ID Y1A9 CLOAB
                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-8BP-2003 (Rel. 42, Last annotation update)
Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-
binding protein 1) (HIV-EP1) (Major histocompatibility complex binding
protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
(PRDII-BP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "High-resolution solution structure of the double Cys2His2 zinc finger from the human enhancer binding protein MBP-1."; Blochemistry 31:3907-2917(1992).

-1- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE 5'-GGGACTTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CRV, OR HIVI, IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I MHC, INTERLEUKIN-2 RECEPTOR, AND INTERPERON-BETA GENES. IT MAY ACT
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "High-resolution three-dimensional structure of a single zinc finger from a human enhancer binding protein in solution."; Blochemistry 29:9324-9334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN T-CELL ACTIVATION.
SUBSELLULAR LOCATION: Nuclear.
INDUCTION: BY MITOGEN AND PHORBOL ESTER.
DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECURNCE FROM N.A.
MEDLINE=90169514; PubMed=2106471;
Fan C.M., Maniatis T.;
Fan C.M., Maniatis T.;
Man DNA-binding protein containing two widely separated zinc finger motifs that recognize the same DNA sequence.";
Genes Dev. 4:29-42(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NWR OF 2087-2142.
MEDLINE-92232684; PubMed-1567844;
Cmichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E. Gronenborn A.M.;
                                                                                                                                                                    ö
                                                                                                                           Score 36; DB 1; Length 1498;
Pred. No. 24;
2; Mismatches 2; Indels
                                                                                     1498 AA; 168968 MW; FF42037A335A9649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 2113-2142.
MEDLINE-91064333; PubMed-2248949;
Omichinski J.G., Clore G.M., Appella B., Sakaguchi K.,
                                                                                                                                                                                                                                                                                                                                      2717 AA.
                                                                     PTSK/SPOILIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC-FINGER IN-BETWEEN.
-!- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                             69.2%;
60.0%;
                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                          |: :| ||||
1276 BQKIPMGMSY 1285
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                       1188
                                                                                                                                                                                                     1 EBVVPXGMSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIVEPI OR ZNP40.
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P15822,
                                                NP BIND
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SEQUENCE
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                                                                                                                                                                                                               "A novel maternally expressed gene, ATP10C, encodes a putative aminophospholipid translocase associated with Angelman syndrome."; Nat. Genet. 28:19-20(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AloC HUMAN STANDARD; PRT; 1499 AA.
O60312; 096514;
30-MAY-2000 (Rel. 39, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
15-SRP-2003 (Rel. 42, Last annotation update)
16-SRP-2003 (Rel. 42, Last annotation update)
(Aminophospholipid-transporting ArPase VC (EC 3.6.3.1) (ATPVC)
ATPLOC OR ATPVC OR KIAA0566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21313119; PubMed=11353404;
Herzing L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.;
"The human aminophospholipid-transporting ATPase gene ATP10C maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh
Oshimura M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 1; Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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2; Mismatches
                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                      Transport; Transmembrane; Glycoprotein.
TRANSMEM 71 91 POTENTIAL.
TRANSMEM 103 123 POTENTIAL.
                                                                                                                                                                                                                     EMBL; MS9167; AAA33615.1; ALT_SEQ.
InterPro; IPRO01902; Sulph_transpt.
Pfam; PR00916; Sulfate_transp; 1.
TIGRFAMs; TIGR00815; SulP; 1.
PROSITE; PS01130; SLC26A; 1.
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66.7%;
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788 AA;
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                                                                                                                           DR GO; GO:0005637; F:DNA binding activity; TAS.

DR GO; GO:0005677; F:DNA binding activity; TAS.

DR DR GO; GO:0005677; F:DNA binding activity; TAS.

DR DR: Fam; PR007087; Zaf C2H2;

DR PROSTTS; PS000028; ZINC FINGER C2H2 1; 4.

DR PROSTTS; PS000028; ZINC FINGER C2H2 1; 4.

DR PROSTTS; PS000028; ZINC FINGER C2H2 2; 4.

CW Transcription regulation; Alocatinger; Metal-binding; DNA-binding;

T ZN FING 406 428

T ZN FING 466 428

T ZN FING 434 456
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Sandal N.N., MarcKer K.A.;
"Similarities between a soybean nodulin, Neurospora crassa sulphate
permease II and a putative human tumour suppressor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and DNA recognition
lfate permease II in
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Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=91129256; PubMed=1825178;
Ketter J.S., Jarai G., Ru Y.-H., Marzluf G.A.;
"Nucleotide sequence, messenger RNA stability, and DNA recogn elements of cys-14, the structural gene for sulfate permease Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 1; Length 2717;
Pred. No. 73;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              297217 MW; D45D3CA951FEA561 CRC64;
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C2HC-TYPE.
C2H2-TYPE.
C2H2-TYPE.
POLY-SER.
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                                                                 PIR; A34203; A34203.
PDB; 3ZNF; 15-JAN 92.
PDB; 4ZNF; 15-JAN-92.
PDB; 1BBO; 31-OCT-93.
TRANSFAC; T00497; -.
Genew; HGNC:4920; HIVEP1.
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2127 2131
2717 AA;
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                                                                                                                                                                                                                                                                                                                                                      DISEASE: Defects in ATP10C are a cause of Angelman syndrome (AS) [MIM:105830]; also known as 'happy puppet syndrome'. It is characterized by features of severe motor and intellectual retardation, microcephaly, ataxia, frequent jerky limb movements and flapping of the arms and hands, hypotonia, hyperactivity, hypotymentation, seizures, absence of speech, frequent smiling and episodes of paroxysmal laughter, and an unusual facies characterized by macrostomia, a large mandible and open-mouthed expression, a great propensity for protruding the tongue ('tongue thrusting'), and an occipital groove.

SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
                                                                                                                      Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
Prediction of the coding sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 5:31-38(1988).
-!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- TISSUB SPECIFICITY: Wide expression, with highest levels in
kidney, followed by lung, brain, prostate, testis, ovary, and
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GO; GO:004012; P:phosphollpid-translocating ArPase activity; NAS.
GO; GO:0004012; P:phosphollpid-translocating ArPase activity; NAS.
GO; GO:000360; P:regulation of cell shape; NAS.
InterPro; IPR00539; P:regulation of cell shape; NAS.
InterPro; IPR00539; P:phosse.
InterPro; IPR005394; Hydrolase.
PERO; PRO0101; CATATPASE.
FRINTS; PR00119; CATATPASE.
TIGRPAMS; TIGR01652; ATPase-Plipid; 1.
TIGRPAMS; TIGR01652; ATPase-Plipid; 1.
TIGRPAMS; TIGR01644; ATPASE BI E2: 1.
PROSITE; PS00154; ATPASE BI E2: 1.
Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
adjacent to UBE3A and exhibits similar imprinted expression."; Am. J. Hum. Genet. 68:1501-1505(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AY029487; AAK33100.1; JOINED.
EMBL; AY029488; AAK33100.1; JOINED.
EMBL; AY029489; AAK33100.1; JOINED.
EMBL; AY029491; AAK33100.1; JOINED.
EMBL; AY029491; AAK33100.1; JOINED.
EMBL; AY029492; AAK33100.1; JOINED.
EMBL; AY029494; AAK33100.1; JOINED.
EMBL; AY029494; AAK33100.1; JOINED.
EMBL; AY029495; AAK33100.1; JOINED.
EMBL; AY029496; AAK33100.1; JOINED.
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                                                                                   TISSUE=Brain;
MEDLINE=98290545; PubMed=9628581;
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                                                               SEQUENCE OF 337-1499 FROM N.A.
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EMBL; AY029501; AAK33100.1; JO
EMBL; AY029502; AAK33100.1; JO
EMBL; AY029503; AAK33100.1; JO
EMBL; AY029503; AAK33100.1; JO
Genew, HGNC:13847; ATP10C.
MIM; 605855; -.
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EMBL; AY029494; AJ
EMBL; AY029495; AJ
EMBL; AY029496; AJ
EMBL; AY029499; AJ
EMBL; AY029499; AJ
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"The complete genome sequence of the murine respiratory pathogen
Mycoplasma pulmonis.";

Nucleic Acids Res. 29:2145-2153 (2001).

-!- FUNCTION: This protein binds directly to 23s ribosomal RNA and is
necessary for the in vitro assembly process of the 50s ribosomal
subunit. It is not involved in the protein synthesizing functions
of that subunit (By similarity).
-!- SIMILARITY: BELONGS TO THE L20P PAMILY OF RIBOSOMAL PROTEINS.
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MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma pulmonis.
Bacteria; Pirmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
POLY-GLU.
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Pred. No. 64;
0; Mismatches 3; Indels
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D4996A4D0635A68D CRC64;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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EXTRACELLULAR (POTENTIAL)
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Best Local Similarity 72.7-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2107;
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ID RL20 MYCPU
AC Q98QV0;
Altigene
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Pred. No. 10;

60.04;

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Best Local Similarity
Matches 6; Conserva
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MEDLINE=98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.B.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Merlavage A.R., Graham D.E., Kyrpides N.C.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%; Score 33; DB 1; Length 165;
                                                                                                                                                                                                         63.5%; Score 33; DB 1; Length 116; 77.8%; Pred. No. 7.1; 1; 1ve 0; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 7 27 27
                                                                                                                                                                      g; Complete proteome.
C59C748901B18F14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BBC17054810ADBF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
           EMBL, AL445563; CAC13434.1; -. PRR; E90544; E90544. Wypul_2610; -. HAMAP, Mr 00382; -; 1. InterPro; IPR005813; L20 act org. InterPro; IPR005812; L20 bact org. If may PP00453; Ribosomal_L20; IPRNNTS; PR00453; Ribosomal_L20; IPRNNTS; PR00062; RIBOSOMALL20. Probom; PD002389; L20; 1.
                                                                                                                                    FIGDON; PUOUSSS; LZU; 1.
TIGRFAMS; TIGRO1032; rplT_bact; 1.
PROSITE; PS00937; RIBOSOWAL LZU; 1
RIBOSOGMAI protein; RNA-binding; C
SEQUENCE 116 AA; 13565 MW; C59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000968; AAB89307.1; -. PIR; D69493.
TIGR; AF1949; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17588 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein AF1949 AF1949.
                                                                                                                                                                                                                            Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                      3 VVPXGMSYS 11
                                                                                                                                                                                                                                                                                                68 VRPLGMSYS 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter J.C.;
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028330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAINSNCTC 11168;
MEDLINE=20150912; PubMed=10688204;
MEDLINE=20150912; PubMed=10688204;
MEDLINE=20150912; PubMed=10688204;
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jasham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jasham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jasham D., Chillingworth T., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";
Nature 403:665-668(2000).
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 160-253 FROM N.A.
STRAIN=ATCC 43431 / TGH 9011;
MEDLINE=55247673; PubMed=7730270;
Hani B.K., Chan V.L.;
"Expression and characterization of Campylobacter jejuni benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Pred. No. 16;
2; Mismatches 2; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; C81374; C81374.
PIR; 140758; 140758.
Hypotherical protein; Complete proteome.
SEQUENCE 253 AA; 29783 MW; P96D3FP3265F8A6A CRC64;
  ٠<u>.</u>
                                                                                                                                                                                                                                                                        P45489; Q9PNVO;
01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTX3 MOUSB

ID CTX3 MOUSE

STANDARD; PRT; 280 AA

C 09D387; 09CXQ4;

DT 28-PBB-2003 (Rel. 41, Created)

DT 28-PBB-2003 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                    253 AA
1; Mismatches
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 177:2396-2402(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL139076; CAB73246.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein Cj0990c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.5%;
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Best Local Similarity 55.00,
  6; Conservative
                                                                                                                                                                                                                                                       STANDARD;
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185 DIPPSGMSY 193
                                                       1 EEVVPXGMSY 10
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                                                                                          60 EESIPDGASY
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SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

STRAIN=C57BL/6J; TISSUB=Embryonic head;
MEDLINE=21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arawaw T., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda S.,
Arawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov G., Quackenbush J.,
Rochim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Havashizaki V., V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUENCE FROM N.A. (ISOFORM 2).

TISSUE-Mammary fibroblast;

MEDINE-238825; PubMed-12477932;

MISUINE-238825; PubMed-12477932;

Altechul S.P., Zeoberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altechul S.P., Zeoberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heigh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheefer B. B., Bonaldo M.F., Casavant T.L., Scheefer T.E., Bromstein M.J., Uddin T.B., Toshiyui S., Carninci P., Prange C., Bromstein M.J., Uddin T.B., Toshiyui S., Carninci P., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worlly M., Sodergren E.J., Lu X., Gibbs R.A., Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Allakealey R.W., Marny D.W., Scheurtz J., Myers R.M., Butkeafley R.W., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Thuman and mouse colly sequences."

Thuman and mouse colly sequences."

Thuman and mouse colly sequences."
                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLUIAR LOCATION: Type I membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
15-SEP-2003 (Rel. 42, Last annotation update)
Protein C20orf103 homolog precursor.
C20ORF103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9D387-1; Sequence=Displayed;
                                                                     Mus musculus (Mouse).
                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=2;
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Gapa

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2; Indels

Score 33; DB 1; Length 280;

280 AA; 31721 MW;

230

CONFLICT CONFLICT SEQUENCE

Pred. No. 18; 0; Mismatches

63.5%;

Query Match Best Local Similarity 75.v-

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(POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL)

PROTEIN C200RP103 HOMOLOG. EXTRACELLULAR (POTENTIAL).

Transmembrane; Signal; Alternative splicing.

EMBL; AKO1822; BAB31124.1; ALT\_FRAMB. EMBL; BCO47791, AALMO4791.1; -. MGD; MGT:1920368; 3110035N03Rik. MGD; MGT:1923411; 6330527006Rik.

BAB29169.1;

CYTOPLASMIC (POTENTIAL)

30 236 257 257 35 102

CARBOHYD CARBOHYD CARBOHYD VARSPLIC CONPLICT

DOMAIN TRANSMEM DOMAIN

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SIGNAL

POTENTIAL.

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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAINEL TOT NIGS61 / Serotype 01;

MEDLINE-20406833; PubMed=10952301;

Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.A.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 406:477-483(2000).
-!- CATALTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate = -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase)
AROA OR VC1732.
                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBUNIT: Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1- SIMILARITY: Belongs to the EPSP synthase family.
                                             426 AA.
                                                                                    28-PBB-2003 (Rel. 41, Created)
                                           STANDARD;
                                                                                                                                                                                                                        cholerae
                                                                                                                                                                                                                                                                                     NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frager C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cholerae.";
                                        VIBCH
                                                             O9KRBO;
RESULT 12
AROA_VIBCH
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IsoId=Q9D387-2; Sequence=VSP\_003820; CAUTION: Ref.1 sequence differs from that shown due to frameshifts in positions 174 and 239.

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genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSR2_HUMAN
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REPUBLICE TROWN N.A.

SEQUENCE FROM N.A.

REPUBLINE=2184401; PubMed=11859360;

RA MEDINE=2184401; PubMed=11859360;

RA MODINE=2184401; PubMed=11859360;

RA WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA BROOKS K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA BROOKS K., Hornsby T., Howarth S., Huckle B., Huckle T., Fraser A.,

COllins M., Connor R., Cromin N., Harris D., Hidalgo J., Hodgson G.,

RA HOLFOYd S., Hornsby T., Howarth S., McDonald S., McLean J.,

RA HOLFOYD S., Mongall K., Murphy L., Niblett D., Odell C.,

Ames K., Jones M., Leather S., McDonald S., McLean J.,

RA Monory P., Woule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Murberford K., Rutter S., Saunders D., Quail M.A., Rabbinowitsch B.,

Rutherford K., Rutter S., Saunders D., Quail M.A., Rabbinowitsch B.,

Rutherford K., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Woodward J., Volckaert G., Aert R., Robben J., GTymonprez B.,

Woodward J., Volckaert E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gableau A., Cadieu E., Direano S., Gloux S., Lelaure V., Mottier S.,

RA Goffeau A., Cadieu E., Direano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gallardin C., Moner K., Hurst S.M.,

Lucas M., Rochet M., Gallardin C., Moner K., Hurst S.,

RA Dagar R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dagar R.R., Cruzado L., Jimenez S., Almstrong J., Forsburg S.L.,

RA Dagar R.R., Cruzado L., Jimenez S.,

RA Dominguez A., Revuelta J.L., Moreno S., Almstrong J., Forsburg S.L.,

ROETURTI L., Lowe T., McCombie M. R., Paulsen I., Potashkin J.,

Cerrutti L., Lowe T., McCombie M. S., Palle I., P.,

Robar S., Revuell B. G., Nurse P.;
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28-FEB-2003 (Rel. 41, Last annotation update)
HSp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (Cell division control protein 37).
                                                                                                                            HAMAP; MF 00210; -; 1.
InterPro; IPR006264; ArcA.
InterPro; IPR001966; BESP syntase.
InterPro; IPR001966; BESP syntase.
Pfam; PP00275; EPSP syntase; 1.
ProDom; PD001867; EPSP syntase; 1.
TIGRFAMS; TIGR01356; arcA; 1.
PROSITE; PS00085; EPSP SYNTHASE 1; 1.
PROSITE; PS00085; EPSP SYNTHASE 2; 1.
Arcmatic amino acid blosynthasis; Transferase; Complete proteome. SEQUENCE 426 AA; 46101 MW; 38852D6483BFEIC3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                     1; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Westwood D.K.; Fantes P.A.; Westwood P.K.; Preston N.C.; Fantes P.A.; "Schizosaccharcomyces pombe cdc37 gene."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetacese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
                                                      EMBL; AE004251; AAF94882.1; -. PIR; D82163; D82163.
                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 60.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 EFVIPAGOSY 232
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NCBI_TaxID=4896;
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MIDLINE-22388257; PubMed=12477932;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moorer T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownsein M.J., Usdin T.B., Toshhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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MEDLINE-20175430; PubMed=10708517;
Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
Portier B.P., Ucki K., Billings S., Ramagwamy S., Mohrenweiser H.W.,
Schatthauer B.W., Louis D.N., Jenkins R.B.;
"A transcript map of the chromosome 19q-Arm glloma tumor suppressor
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Nature 415:871-880 (2002).

-!- FUNCTION: With Hsp90 it forms a complex that binds to several kinases, resulting in stabilization and promotion of their activity (By similarity).

-!- SUBUNIT: Forms a complex with Hsp90. Interacts with a number of kinases (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: BELONGS TO THE CDC37 FAMILY.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Q9NZM5; Q9BTC6; Q9HAX6; Q9NPP1; Q9NPR4; Q9UF12;
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 42, Last sequence update)
15-SRP-2003 (Rel. 42, Last annotation update)
Glioma tumor suppressor candidate region gene 2 protein (p60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.5%; Score 33; DB 1; Length 466; 50.0%; Pred. No. 30; ive 2; Mismatches 3; Indels
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InterPro; IPR004918; Cdc37.
Pfam, PF03234; Cdc37; Ccc37; Ccc37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ132377; CAB38758.1; -. EMBL; AJ132376; CAB38757.1; -. EMBL; AL049769; CAB42371.2; -.
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Matches 5; Conservative
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98 DSAIPGGMSY 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; T43653; T43653
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBUNIT: Interacts with HSV-1 early proteins ICP22 and ICP0.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- TISSUB SPECIFICITY: Expressed at high levels in heart and pancreas, moderate levels in placenta, liver, skeletal muscle, and kidney, and low levels in brain and lung.
-1- SIMILARITY: BELONGS TO THE GLYSCR2 PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR 011486.

605 -> HG (IN REF. 2; AAH04229).

G -> R (IN REF. 3).

RRKEQLWEKLAKGGELPREVRRAQARLLAPSATRAKPGPQD

TYTERP -> SGRSZYCKRSWERRASSPCGAAGPSPVAQPFCN

KGPNAPCHALAA (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A -> S (IN REF. 2; AAH04229).
D -> H (IN REF. 3).
PEGNILADRFKSFORRNMIEPRERAKFKRYKYKKLVEKAF
REIQ -> VLTVPRFSPORPWIPSLLPVPPRGYGHHGCP
WAGFVGPMPRG (IN REF. 5).
EGNILRDRFKSFORRNMIEPRERAKFKRKYKVKLVEKRFR
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                    SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=99214318; PubMed=10196275;
Bruni R., Fineschi B., Ogle W.O., Roizman B.;
"A novel cellular protein, p60, interacting with both herpes simplex virus 1 regulatory proteins ICP22 and ICP0 is modified in a cell-type-specific manner and is recruited to the nucleus after infection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIQL -> RGQHSFETGSRAFRGGI (IN REF. 3)
7F18923E348CB52B CRC64;
                                                                                                                                                                                                                                                                                                                                                                  Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                               SEQUENCE OF 12-478 FROM N.A.
Andreu N., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0008181; F:tumor suppressor; TAS.
Nuclear protein; Polymorphism.
VARIANT 389 389 R -> Q.
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EMBL; AF296124; AAH10095.1; --
EMBL; AL359315; CAB94786.1; --
EMBL; AL359315; CAB94787.1; --
EMBL; AL359315; CAB94787.1; --
EMBL; AL359316; CAB94787.1; --
EMBL; AL359316.3; CAB94787.1; --
SWISS-2DPAGE; Q9NZM5; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF182076; AAF62873.1; -. EMBL; BC004229; AAH04229.1; -.
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                                                                                                                                                                                                                                                     J. Virol. 73:3810-3817(1999).
                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 218-477 FROM N.A.
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417
433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garnier T., Cole S.T.;
Complete nucleotide sequence and genetic organization of the
bacteriorinogenic plasmid, pIP404, from Clostridium perfringens.";
Plasmid 19:134-150(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garnier T., Cole' S.T.;
"Characterization of a bacteriocinogenic plasmid from Clostridium Characterization of a perfringens and molecular genetic analysis of the bacteriocin-encoding gene.',
J. Bacteriol. 168:1189-1196 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid p1P404.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Score 33; DB 1; Length 478;
Pred. No. 31;
                                                  3; Indels
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96699 MW; F4E5E8971C31C6C6 CRC64;
                                                                                                                                                                                                                                                                                                                 (Rel. 06, Created)
(Rel. 06, Last sequence update)
(Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                    890 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ol. Microbiol. 2:607-614(1988).
1- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
                                               1; Mismatches
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Pred. No.
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InterPro; IPR003646; SH3 bac.
InterPro; IPR000834; Zn_CarbOpept.
Pfam; PP00246; Zn_CarbOpept; I.
SWART; SM00287; SH3b; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88336297; PubMed=2901768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89039249; PubMed=2460717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - INDUCTION: By UV irradiation.
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63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M14481; AAA98248.1; -.
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66.7%;
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                                               6; Conservative
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium perfringens.
                                                                                                                                          239 EVAPAGASYN 248
                                                                                             2 EVVPXGMSYS 11
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                    Best Local Similarity
Matches 6; Conserv
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01-JAN-1988 (Rel.
01-OCT-1994 (Rel.
Bacteriocin BCNS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1502;
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BCNS_CLOPE
ID BCNS_CLOPE
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0; Gaps

2; Indels 1; Mismatches 6; Conservative 2 EVVPXGMSY 10 ||||| :: 170 EVVPGGFTY 178 Matches ઠે g

Search completed: December 22, 2003, 17:42:26 Job time : 4.6 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 22, 2003, 17:27:26 ; Search time 25.2 Seconds (without alignments) 112.642 Million cell updates/sec Run on:

US-09-909-164-10 52 1 BEVVPXGMSYS 11

Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 23:\* Database :

sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\*
sp\_organelle:\*
sp\_phage:\* unclassified:\* \_rvirus:\* 8p\_virus:\*
sp\_vertebrate:\* sp\_bacteriap:\* sp\_archea:\* sp\_bacteria:\* sp plant:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

#### SUMMARIES

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	Description	Q8dih0 synechococo	Q98fx1 rhizobium	O74056 cenarchaeum	Q9ury8 schizosacch	Q8ewd4 mycoplasma	Q8r126 mus musculu	Q8vd18 mus musculu	Q8btx4 mus muscul	Q8bk35 mus muscul	Q40129 lycopersico	Q9xvk4 caenorhabdi	Q8cld7 mus musculu	043733 homo sapien	Q9bh83 plasmodium	Q9bha5 plasmodium	Q81587 plasmodium
	ID	Овріно	Q98FX1	074056	Q9URY8	Q8EWD4	Q8R126	Q8VD18	Q8BTX4	Q8BK35	040129	Q9XVK4	Q8C1D7	043733	09внв3	Q9BHA5	081557
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	Query Aatch Length DB	1044	387	3472	840	1123	471	484	484	484	225	425	495	. 956	583	583	583
ф	Query Match	75.0	73.1	73.1	71.2	71.2	69.5	69.5	69.3	69.2	67.3	67.3	67.3	67.3	67.3	67.3	67.3
	Score	39	38	38	37	37	36	36	36	36	35	35	35	35	35	35	35
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Q01487 rattus ratt Q8pmi6 xanthomonas Q8pm2t xanthomonas Q9pdmc xylella fas Q14122 homo sapien Q12479 saccharomyc Q97182 sulfclobus Q28342 archaeoglob Q96mul homo sapien Q92mdc rhizobium m Q81ym3 homo sapien Q92mc rhizobium m Q81ym3 homo sapien Q92mc rhizobium m Q81ym3 homo sapien Q94x45 bifdobacte Q8xt05 ralstonia s	
Q01487 Q8PM16 Q8PM16 Q9PDM6 Q14122 Q14124 Q14124 Q14124 Q14126 Q14126 Q14136 Q18PP5 Q1	
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## ALIGNMENTS

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Gaps
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Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Nakamabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokwa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002).
ENBL; APO05374; BAC09170.1; -.
Complete proteome.

SKGUENCE 1044 AA; 113205 MW; 00E9C13F0P636D2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                           (TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                        PRT; 1044 AA
                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq.
01-MAR-2003 (TrEMBLrel. 23, Last ann
Multidrug efflux transporter.
TLL1618.
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                   PRELIMINARY;
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853 |||:| |: || 843 EEVLPNGIGYS

1 BEVVPXGMSYS 11

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PRT; PRELIMINARY; RESULT 2 Q98FX1 ID Q98FX1

387 AA.

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Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshimo C., Horimo A., Shiba T., Sasaki T., Hattori M.;
The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
EMBL, AD004171; BAC44062.1;
Complete proteome.
SEQUENCE 1123 AA; 123636 MW; AAD707330E3DB4AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Aunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AL132779; CABGOUS-1; --
GeneDB SPONDe; SPACBG-0.55; --
InterPro; IPRO12645; STAS.
InterPro; IPRO1302; Sulph_transpt.
Pfam; PPO1340; Sulfate transp; 1.
Pfam; PPO0316; Sulfate transp; 1.
PRONSITE; PSSG081; STAS; 1.
PROSITE; PSSG081; STAS; 1.
SEQUENCE 840 AA; 93517 MW; ED4833E162B69077 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=28227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.2%; Score 37; DB 16; Length 1123; 70.0%; Pred. No. 70; ive 1; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.2%; Score 37; DB 3; Length 840; 77.8%; Pred. No. 51; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Flasion yeast).
Bukaryota, Pungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetacese;
Schizosaccharomyces.
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Last annotation update)
                                                                                                  840 AA
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                                                                                                                                 01-WAY-2000 (TrEMBLrel. 13, 01-WAY-2000 (TrEMBLrel. 13, 01-WAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                              Probable sulfate permease.
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  2294 EDVIPRGISFS 2304
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658 EYVPMGLSYS 667
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MYPE2710.
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                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=972h-;
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QBEND4;
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EMBL: AR083072; ARC62699.1; -.
InterPro; IPR000515; BPD transp.
InterPro; IPR001680; WD40.
PFam; PF00400; WD40; 4.
                                                                                                                                                                                                                                                                            Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Simpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Simpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Simpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Simpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Simpo S., Sugimoto M., DNA Res. 7:31-338(2000).

EMBL; AP003002; BAB50445.1; -.
InterPro; IPR00293; Peptidase M.20.
Pfam; PF01546; Peptidase M.20.
Pfam; PF01546, Peptidase M.20; I.
Hydxolase; Complete protecome.
SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;
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MEDINE=98422450; PubMed=9748430;
Schlebger C. DeLong B.F., Preston C.M., Feldman R.A., Wu K.Y.,
Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 73.1%; Score 38; DB 16; Length 387; Local Similarity 60.0%; Pred. No. 13; 16 Conservative 2; Mismatches 2; Indels
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                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00320; WD40; 2.
PROSTIR; PS00402; BPD TRANSP_INN MEMBR; 1.
Hypothetical protein; Repeat; WD repeat.
SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 367,1 kDa protein.
                    (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 18, Last annotation update)
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                                                                                                                     Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                           MEDLINE=21082930; PubMed=11214968;
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367 DEAIPHGMSY 376
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                                                                               Hippurate hydrolase.
MLR3583.
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Matches 6: Conserv
                                                                                                                                                                                                  [1] SEQUENCE FROM N.A. STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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NCBI_TaxID=46770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O74056
O74056;
01-NOV-1998 (
                    01-0CT-2001
01-0CT-2001
                                                          01-OCT-2001
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Matches
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Similar to glioma tumor suppressor CANDIDATE region gene
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                            protein.
Mus musculus (Mouse)
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                                                                                                                                                      NCBI_TaxID=10090;
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Q8BK35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
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Matches
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                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to glioma tumor suppressor candidate region gene 2.
GLTSCR2 OR AW536441.
Buts musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
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Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 11; Length 484;
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
Straubberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025810; AAH25810.1; -.
MyDD; MGT:2154441; Gltscr2.
Hypochhetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                         471 AA.
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                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequenc
01-MAR-2003 (TrEMBLrel. 23, Last annotat
Hypothetical 54.5 kDa protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                      PRELIMINARY;
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EVIPAGASYN 248
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TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EVVPXGMSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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01-MAR-2003
01-MAR-2003
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QBBTX4;
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Q8VD18;
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                                                      RESULT 6
Q8R126
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GROUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.;
Nature 420:563-573(2002).
SMBL; AKO88461; BAC40367.1; -
SRQUENCE 484 AA; 55806 MW; B3056425B5EECAD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Pituitary;
MEDLINE222346893; PubMed=12466851;
The FANTOM Consortium.
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2996 (TrEMBLrel. 23, Last annotation update)
Mypothetical 25.2 kDa protein precursor.
Lycoperation esculantum (Tomato).
Lycoperation (Triadiolantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI _TaxID=10090;
Bukaryotala (mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinee, Mus.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to glioma tumor suppressor CANDIDATE region gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK077341; BAC36760.1; -.
SEQUENCE 484 AA; 55792 MW; BB67949BCBB92D44 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last seq
01-WAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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239 EVIPAGASYN 248
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239 BVIPAGASYN 248
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Q40129
AC Q4012
AC Q4012
DT 01-NO
DT 01-NO
DB HYPOLE
OS LYCOP
OC SUKAT
OC ARTER
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Head;

STRAIN=22536483; PubMed=12466851;

The FANTOM Consortium
the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs.";

Nature 420:563-573 (2002).

EMBL; AK028258; BAC25846.1; -.

SEQUENCE 495 AA; 55358 MW; B6A22A093C114752 CRC64;
                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
DNA binding protein (Fragment).
DN451B15.2.
Bune asplene (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCTI.
Plasmodium falciparum.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 11; Length 495;
Pred. No. 75;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.3%; Score 35; DB 4; Length 556; 66.7%; Pred. No. 86; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tubby B.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; Z98050; CAB10847.1; -. NON TER 1 SEQUENCE 556 AA; 59059 MW; ECB00E4033FB2528 CRC64;
                               01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
CDNA F131891 FIS.
Mus musculus (Mouse)
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Last annotation update)
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 495 AA
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                           63.64;
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.6
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Best Local Similarity 66.7
Matches 6; Conservative
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Rhabditidae, Peloderinae, Caenorhabditis.
                             SEQUENCE FROM N.A.

STAIN-FP36; TISSUE-Pistil;

K MEDLINE-95375231; PubMed=7647301;

Milligan S.B., Gasser C.S.;

"Nature and regulation of pistil-expressed genes in tomato.";

I Plant Mol. Biol. 28:691-711(1995).

E RMEJ, UZ0592; AAA80497.1; -.

R InterPro; IPR002160; Kunitz_legume.

R Pfant, Pr00197; Kunitz_legume.

R Pfant, Pr00197; Kunitz_legume; 1.

R PRINTS; PR00291; Kunitz_legume; 1.

R PRODINT; SW00453; STI; 1.

R PROSITE; PS00283; SOYBEAN KUNITZ; 1.

H Hypothetical protein; Signal.
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Pred. No. 32;
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018 (1998).
Science 282:2012-2018 (1998).
EMBL; Z81109; CAB0241.1;
WormPep; R10D12.10; CE12690.
InterPro; IPR000719; Prot kinase.
Pfam; PP00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
ATP-binding; Transferase.
SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
                                                                                                                                                                                                                                                                                                    CHAIN 21 225 UNKNOWN.
SEQUENCE 225 AA; 25188 MW; 1074C261D20CFDAD CRC64;
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Last annotation update)
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MEDLINE=99069613; PubMed=9851916;
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Caenorhabditis elegans.
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 NCBI_TaxID=4081;
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Plasmodium falciparum.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
N.CBI_TaxID=5833;
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Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;
Plasmodium falciparum choline transporter (PfSCT1) gene.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY007372; AAK14816.1; -.
EMBL; AX007372; AAG17947.1; -.
InterPro; IPR002123; Acyltransferase.
Pfam; PP01553; Acyltransferase; 1.
SMART; SM00563; PlEC; 1.
SEQUENCE 583 AA; 66917 MW; 2B2BFAE3E395E049 CRC64;
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67.3%; Score 35; DB 5; Length 583;
Best Local Similarity 55.6%; Pred. No. 90;
Matches 5; Conservative 3; Mismatches 1; Indels
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Search completed: December 22, 2003, 17:51:29 Job time : 25.2667 secs

227 IIPVGLSYS 235

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Hepatitis Hepatitis

c virus c virus c virus c virus c virus c virus

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Run on:

Sequence:

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Result No.

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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virucide.
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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| SIDSI/gcgdata/geneseqg-embl/AA1981.DAT:*
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Compugen Ltd.
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/note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                                                                          The sequence represents a peptide compound of the invention having heppatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                  Gaps
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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100.0%; Pred. No. 0.00053;
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                                                                      Claim 17; Page 64; 69pp;
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                                                                                                                                                                                                                                                       The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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virucide.
                                                                                                                                                compound having hepatitis C virus protease inhibitory
ul for treating disorders associated with hepatitis C
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Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                          Brunck TK;
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                                                                                                                                                                                                                       Claim 17; Page 64; 69pp; English.
                                                                                                                                                                     useful for treating
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   21-JUL-2000; 2000US-220101P.
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EEVVPXGMHYS 11
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                                      (CORV-) CORVAS INT INC
                                                                            Levy OE,
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                                                                                                              WPI; 2002-361643/39
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                                                                                                                                                                                         virus protease
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is useful for treating disorders associated with hepatitis C virus.
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                                                                                 1 REVVPXGMHYS
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Best Local Similarity
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                                                   Similarity
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                      Sequence
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                               pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture a medicament to treat disorders associated with HCV protease. A
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ty useful for treating disorders associated with hepatitis C
protease
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                                                                               96.4%; Score 54; DB 23; Length 11;
100.0%; Pred. No. 0.00053;
.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a
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                                                                                                    11; Conservative
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Modified-site
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                                                                                                                                                                                                                                                                                                               Synthetic
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"Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17
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DB 23; Le..
                    11;
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Pred. No. 0.0051;
0; Mismatches 1;
                                                             Mismatches
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                  Score 54;
Pred. No.
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  96.4%; Scc...
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90.9%;
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                                                             Conservative
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ਨੇ 셤 08-OCT-2002

ABB80541;

Synthetic virucide.

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
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                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #26.
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Pred. No. 0.008;
0; Mismatches 1
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              ABB80546;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #21.
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Pred. No. 0.0051;
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EEVVPXGMHYS
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Modified-site
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Lim-wilby M,

31-JAN-2002

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Gaps

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ABB80546 standard; peptide; 11 AA.

RESULT 7 ABB80546 ID ABB8

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Sequence Query Match

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/note=
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                                                                                                                                  (CORV-) CORVAS INT INC
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   Misc-difference
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                                                           "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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virucide.
                                                                                                                                                                                                                                                                           Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #34.
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Pred. No. 0.008;
0; Mismatches 1; Indels
                                        'note= "N-terminal acetyl"
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                                                                                                            /note= "C-terminal amide"
                                                                                        'note= "D-form residue"
                    Location/Qualifiers
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90.9%;
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BEVVPXGSHYS 11
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                                                                                                                                                                                                                                    Levy OE,
                                                                                                                                                                                                              CORV-) CORVAS INT INC
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                                                                                                                               WO200208251-A2
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Modified-site
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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Pred. No. 0.008;
0; Mismatches 1; Indels
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                                                       /note= "C-terminal amide"
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/note= "D-form residue"
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90.9%;
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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    residue 7"
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                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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                                                                                                                                                                                                                                                                                                                Score 46; DB.23; Length 11;
Pred. No. 0.02;
0; Mismatches 1; Indels
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                                                                                                                Claim 17; Page 64; 69pp; English.
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ilarity 90.9%;
Conservative
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Best Local Similarity
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               WPI; 2002-361643/39.
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                                                                                                                                                                                                                compound having hepatitis C virus protease inhibitory
al for treating disorders associated with hepatitis C
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Pred. No. 0.008;
0; Mismatches 1; Indels
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                                                                                                                                                 Levy OE,
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ABB80531;

ABB80531

RESULT 11 ABB8053

Sequence

Novel

Query Match

Matches

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Gaps

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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residue 7"
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0
                                                                                                                                                                  Score 46; DB 23; Length 11;
Pred. No. 0.02;
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90.9%;
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                                                                                                                                                                                   Local Similarity
                                                                                                                                       11 AA;
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                                                                                                                                                                                                                                                                                                                                           carbonyl forming keto-amide linkage with
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Score 45; DB 23;
Pred. No. 0.031;
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residue 7"
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                   /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
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Pred. No. 0.031;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                             'note= "D-form residue"
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              ABB80524 standard; peptide; 11 AA.
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Best Local Similarity 90.9
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                                          ABB80524;
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Search completed: December 22, 2003, 17:41:01 Job time : 32.4667 secs

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Sequence 4794, Ap
Sequence 21444, A
Sequence 19, Appl
Sequence 2, Appli
Sequence 26615, A
Sequence 27834, A
Sequence 27834, A
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                                                                                                                                                                                                                                                                        December 22, 2003, 16:37:03 ; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
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(c) 1993 - 2003 Compugen Ltd.
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US-09-252-991A-21444
US-08-821-119-19
US-08-821-118-2
US-08-252-991A-26615
US-09-252-991A-27834
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US-08-810-988A-23
US-08-810-988A-3
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Sequence 4794, Application US/09134001C

Sequence 4794, Application US/09134001C

Refeart No. 6380370

GRNERAL INFORMATION:

GRNERAL INFORMATION:

GRNERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCT TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCT TITLE OF INVENTION: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR PLING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2144.4 Application US/09252991A

Sequence 2144.4 Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21444
LENGTH: 886
TYPE: PRI
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          US-08-464-517-23
US-08-246-361A-5
US-08-246-361A-23
US-08-463-772-23
US-07-947-120-8
US-08-472-893A-8
US-08-460-694-2
US-08-461-517-19
US-08-246-361A-19
                                                                                                                                                                                               -07-667-711B-2
                                                                                                                                                                                  US-08-460-744-2
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US-08-947-492-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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199 KEVVSNGLHYS 209
                        1 EEVVPXGMHYS 11
RESULT 2
US-09-252-991A-21444
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ORGANISM:
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APPLICANT: Holm, Kaj Andre
APPLICANT: Rasmussen, Grethe
APPLICANT: Rasmussen, Grethe
APPLICANT: Halkier, Torben
APPLICANT: Lehnbeck, Jan
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
VORRESPONDENCES: 23
CORRESPONDENCES: ADDRESS:
ADDRESSEE: No. 58211040 No. 5821104disk of No. 5821104th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                        Gaps
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                                                   Score 37; DB 4; Length 856;
Pred. No. 40;
0; Mismatches 3; Indels
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM:
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
CLASSIFICATION: 435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Patent No. 5821104
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US-08-821-118-2
US-08-821-118-2
Sequence 2, Application US/08821118
Patent No. 5989889
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rey, Michael APPLICANT: Golightly, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Rias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.7%;
75.0%;
                                                   Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 600 amino acida
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 75.0
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COMPUTER READABLE FORM:
                                                                                                                                                           64 EAVVPGGEHY 73
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Sequence 26515, Application US/0925291A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
CURRENT PILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
PRIOR PRILING DATE: 1998-02-18
PRIOR PRILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

LENGTH: 277
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TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING TRIPEPTIDE AMINOPEPTIDASE
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER. NO. 59898890 No. 5989889disk of No. 5989889th America, Inc. STREET: 405 Lexington Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                         COUNTY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DOS STEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 33,728
TRELECOMMUNICATION INFORMATION:
TELEBHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 2; Pred. No. 1e+02
0; Mismatches
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26615
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75.0%;
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
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Patent NO. 5856161
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Foc Its Use
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCES. 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                         57.1%; Score 32; DB 4; Length 70; 62.5%; Pred. No. 24;
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MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
SOFTARRE: Microsoft Word for Macintosh
SOFTARRE: Microsoft Word for Macintosh
SOFTARRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REPERENCE/DOCKET NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1713-777-2321
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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om: internal
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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STATE: Texas
COUNTRY: USA
ZIP: 77071
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US-08-580-988A-23
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                                                                                                                                         Sequence 27834, Application US/09252991A
Patent No. 6551794
Patent No. 6551794
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27834
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Patent No. 6380362

GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Watson, James D
TITLE OF INVENTION: Polynucleotides and methods for their use.
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050U1
CURRENT PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72

SOFTWARE: FREESEQ for Windows Version 4.0
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Pred. No. 1e+02;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27834
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71.4%;
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Best Local Similarity 44.4%;
Matches 4; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
      1 BEVVPXGMHYS 11
                                                 48 EETVPGGGHTS 58
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627 PGCLHYS 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Rat
US-09-724-864-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-724-864-36
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LENGTH: 747
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Hillman, Jennifer L.
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 APPLICANT:
                                                                                                                                                   STATE:
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Pred. No. 46;
1; Mismatches 2; Indels
                                    Length 102;
                                                                    3; Indels
                                                                                                                                                                                                           Sequence 3, Application US/08879995A
Fatent No. 598566
GENERAL INFORMATION:
APPLICANT: Hilland, Jennifer L.
APPLICANT: Hilland, Jennifer L.
APPLICANT: ARBET, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZUP. 1943 USA
ZUP. 1943 USA
ZUP. 1943 USA
ENDIUM TYBE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DAY
SOFTWARE: PRESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,995A
FILING DATE: Herewith
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGENT INPORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
TELEPHONE: 415-855-0555
                                   57.1%; Score 32; DB 2; 60.0%; Pred. No. 37; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09215096
Patent No. 6008194
GENERAL INFORMATION:
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 126 amino acide TYPE: amino acid STRANDEDNESS: single
                   Query Match
Best Local Similarity 60.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.1
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                     1 EEVVPXGMHY 10
                                                                                                                                   24 BEVFPLAMNY 33
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28 EQVVPGGGH 36
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LIBRARY: General
Targ: 163590
                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
   US-08-580-988A-23
                                                                                                                                                                                    RESULT 10
US-08-879-995A-3
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| Patent No. 5858655
| GENERAL INFORMATION:
| APPLICANT: Arnold, Andrew | TITLE OF INVENTION: PRADI Cyclin and its CDNA | NUMBER OF SEQUENCES: 8
| CORRESPONDENCE ADDRESS: ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 | CITY: Washington | STATE: DC | COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.1%; Score 32; DB 3; Length 126; 66.7%; Pred. No. 46; 2; Indels 1; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 1174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: PESTSEE (TO WINDOWS Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDMESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                               COUNTRY: USA
ZIF: 94304
COMPUTER READALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
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28 EQVVPGGGH 36
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CLONE: 163590
US-09-215-096-3
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20 BEVPPLAMNY 29

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RESULT 14
US-07-667-711B-4
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Patent No. 6107541

GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTON: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & FOX P.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington
STATE: DC
COUNTRY: USA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: END FO Compatible
COMPUTER: Floppy disk
COMPUTER: END FO Compatible
CORRANTIG SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-JUN-1995
CLEASIFICATION: 435
ATTORNEY/AGRAT INFORMATION:
NAME: MCCOnathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFREMENCE/DOCKET NUMBER: 35,279
REFREMENCE/DOCKET NUMBER: 36,279
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERANDE: 202-371-2640
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
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                                                                           ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: TYPE: peptide
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIPICATION: 435
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MOLECULE TYPE: peptide
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APPLICANT: WEBSTER, KEVIN R.
APPLICANT: WEBSTER, KEVIN R.
TITLE OF INVENTION: PSPTIDE INHIBITORS OF THE P33CDK2 AND
TITLE OF INVENTION: P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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US-07-567-711B-4

US-07-567-711B-4

INCORATION 6.110700

FARENT NO. 6.110700

GENERAL INFORMATION: Pradi Cyclin and Its CDNA TITLE OF INVENTION: Pradi Cyclin and Its CDNA TITLE OF INVENTION: Pradi Cyclin and Its CDNA TITLE OF INVENTION: Pradi Cyclin and Its CDNA CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 152;
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Pred. No. 57;
1; Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSER: RRED & ROBINS
STREET: 615 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08193977
Patent No. 5625031
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 57.1
Best Local Similarity 60.0
Matches 6; Conservative
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December 22, 2003, 16:40:14; Search time 20.8667 Seconds (without alignments) 98.451 Million cell updates/sec
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2. (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
3. (cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3. (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5. (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6. (cgn2_6/ptodata/2/pubpaa/PUBCOMB.pep:*
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9. (cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
9. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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1 REVVPXGMHYS 11
                           Copyright
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                     Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

# No. Score March Length DB ID Description 1 33 58.9 273 12 US-10-094-749-2319 Sequence 2319, Ap 2 273 12 US-10-094-749-2319 Sequence 126, App 4 33 58.9 567 15 US-10-270-333-126 Sequence 126, App 5 273 12 US-10-270-333-126 Sequence 126, App 6 33 58.9 3472 12 US-10-029-120-4 Sequence 4, Appli 6 33 58.9 3472 14 US-10-029-120-4 Sequence 4, Appli 8 33 58.9 3472 14 US-10-034-623-4 Sequence 4, Appli 9 32 57.1 236 12 US-10-199-820-21 Sequence 2014, Appli 10 32 57.1 236 12 US-10-199-820-21 Sequence 2016, Appli 11 32 57.1 242 12 US-10-199-820-24 Sequence 2016, Appli 13 2 57.1 254 9 US-094-749-2076 Sequence 2016, Appli 13 2 57.1 254 9 US-094-749-2076 Sequence 2016, Appli 13 2 57.1 254 9 US-09-19-430-241 Sequence 53, Appli 13 2 57.1 258 9 10 US-10-129-80-2076 Sequence 54, Appli 14 32 57.1 289 10 US-10-129-4497-54 Sequence 54, Appli 15 32 57.1 289 10 US-10-124-97-54 Sequence 27, Appli 15 32 57.1 289 10 US-10-024-97-54 Sequence 27, Appli 15 32 57.1 289 14 US-10-024-06-2

TYPE: PRT

ORGANISM: Homo sapiens
US-10-094-749-2319

Sequence 4, Appli Sequence 275, App Sequence 1315, Appli Sequence 164, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 15, Appli Sequence 17, Appli Sequence 13, Appli Sequence 22, Appli Sequence 22, Appli Sequence 111, Appli Sequence 13613, Appli Sequence 13613, Appli Sequence 13613, Appli Sequence 13613, Appli Sequence 13613, Appli Sequence 1697, Appli	
4 US-10-024-066-4 2 US-10-116-275-275 2 US-09-75-1115 2 US-09-756-736-14 1 US-09-934-455-164 2 US-09-736-24 2 US-09-736-24 2 US-09-736-24 2 US-09-75-164 2 US-10-302-267-36 1 US-09-255-088-15 1 US-09-252-088-15 2 US-10-340-792-16 1 US-09-252-088-15 2 US-09-88-480-17 1 US-09-986-480-17 4 US-09-986-480-17 4 US-09-986-480-17 4 US-09-9815-242-13499 US-09-815-242-13499 US-09-815-242-13499 US-09-815-242-13499 US-09-815-242-13499 US-09-815-242-13499 US-09-915-242-13499	ALIGNMENTS US/10094749 41A1  YASU II
57.1. 289 125.7.1. 289 125.7.1. 289 125.7.1. 289 125.7.1. 289 125.7.1. 289 125.7.1. 289 125.7.1. 289 125.7.1. 289 125.7.1. 289 255.4 256.2 847 125.7.1. 285.4 256.2 847 125.7.1. 285.4 256.2 847 125.7.2 855.4 256.2 847 155.7.2 855.4 256.2 847 155.7.2 855.4 256.2 847 155.7.2 855.4 256.2 847 155.7.2 855.4 256.2 855.2 855.4 256.2 855.4 256.2 855.2 855.4 256.2 855.2 855.4 256.2 855.2 855.4 256.2 855	Cation UG 03021974, TAKAO A, TOMOYI TESUJI SU, AI TROYUKI SHIZUKO O, JUN-IC YUUKO O, JUN-IC YOTAKO MA, ICHII AACHIKO MA, ICHII AACHIKO MA, TSUTK NOVEL FI I, KENJI I, KENJI I, KENJI I, KENJI I, KENJI I, KENJI I, KENJI I, KENJI I, KENJI I, KENJI UMBER: 61 2002-01-09-1 2001-09-1 SI 3381
116 222 222 223 224 225 226 227 228 232 232 232 233 233 233 234 234 235 231 235 231 236 231 237 231 237 231 237 237 237 237 237 237 237 237 237 237	RESULT 1  US-10-094-749-2319  Sequence 2319, Applic; Publication No. US200 GENERAL INPORMATION: APPLICANT: SUGITANA, APPLICANT: SUGITANA, APPLICANT: SATO, HI APPLICANT: SATO, HI APPLICANT: SATO, HI APPLICANT: SATO, HI APPLICANT: SATO, NO. APPLICANT: SATO, NO. APPLICANT: SATO, NO. APPLICANT: TAMENIN, APPLICANT: TAMEGHIK, APPLICANT: TAMEGHIK, APPLICANT: TAMEGHIK, APPLICANT: TAMEGHIK, APPLICANT: TAMEGHIK, APPLICANT: MAGHIK, BRICK FILING DATE: 2 NUMBER OF SEQ ID NOS SOFTWARE: PALENTIN VI FRIOR FILING DATE: 2 NUMBER OF SEQ ID NOS SOFTWARE: PALENTIN VI FRIOR FILING DATE: 2 NUMBER OF SEQ ID NOS SOFTWARE: PALENTIN VI FRIOR FILING DATE: 2 NUMBER OF SEQ ID NOS SOFTWARE: PALENTIN VI FRIOR FILING DATE: 2 NUMBER OF SEQ ID NOS SOFTWARE: PALENTIN VI FRIOR FILING DATE: 2 FRIOR FILING

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; TYPE: PRT; Corynebacterium glutamicum US-09-738-626-4919
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; ORGANISM: Cenarchaeum symbiosum
US-10-029-120-4
                                                                                                            Query Match 58.9%;
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                     1 BEVVPXGM--HY 10
                                                                                                                                                                                                                                46 BRIIPIGVPNHY 57
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Matches 5; Conserv
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ORGANISM: Rat
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US-10-029-120-4
LENGTH: 622
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TITLE OF INVENTION: 1SOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: 1SOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
THE REPERBNES: CLOOO733CON
CURRENT APPLICATION NUMBER: US/10/270,333
CURRENT PILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 198
SOFTWARE: FARESEQ FOR Windows Version 4.0
SEQ ID NO 126
LENGTH: 567
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                Query Match 58.9%; Score 33; DB 12; Length 273; Best Local Similarity 71.4%; Pred. No. 1.7e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MAKAGAMA, SATOSHI
APPLICANT: MAKAGAMA, SATOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEBA, MAGATO
APPLICANT: IKEBA, MAGATO
APPLICANT: OZAKI, AKIHIRO
APPLICANT: OZAKI, ANIO
ITIER EFFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4919, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      Sequence 126, Application US/10270333
Publication No. US20030092124A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.9
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                           | |:|||
151 PGGLHYS 157
                                                                                                                 5 PXGMHYS 11
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Sequence 4, Application US/10029120
| Bequence 4, Application US/10029120
| Publication No. US20030175708A1
| GENERAL INFORMATION:
| APPLICANT: Swanson, Rohald V. |
| APPLICANT: Schleper, Christa |
| TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM |
| FILE REFERENCE: DOORP.002A |
| FURRENT APPLICATION NUMBER: US/10/029,120 |
| PRIOR PILING DATE: EARLIER PELING DATE: 1999-09-29 |
| PRIOR PILING DATE: EARLIER FILING DATE: 1999-09-29 |
| NUMBER OF SEQ ID NOS: 123 |
| SEQ ID NO 4 |
| LENGTH: 3472
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                                                                                                                                                                                                                                      US-09-866-050A-663

i Sequence 663, Application US/09866050A

j Sequence 663, Application US/09866050A

j Publication No. US20030040471A1

GENERAL INFORMATION:

APPLICANT: Strachan, Lorna

APPLICANT: Strachan, Mathew

APPLICANT: Murison, James G.

APPLICANT: Rumble, Kane

APPLICANT: Rumble, Kane

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: Compositions of Their Use

FILE REPRENCE: 11000.1011c4U

CURRENT FILIAG DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 725

SOFTWARE: PastSEQ for Windows Version 4.0

1, PARTER OF 1000.1011c4U
Score 33; DB 10; Length 622;
Pred. No. 4.1e+02;
3; Mismatches 1; Indels
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RESULT 10
US-10-029-386-32076
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APPLICANT: Swanson, Robert A.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT FILING DATE: 2011-12-21
PRIOR APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: EARLIER FABLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SMANION.
APPLICANT: SMANION.
APPLICANT: Feldman, Robert A.
APPLICANT: SMANION: NUCLEIC A.
TITLE OF INVENTION: NUCLEIC A.
TILLE REFERENCE: DCORP.002A
CURRENT PELING DATE: 1999-109-29
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
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Pred. No. 2.6e+03;
4; Mismatches 2; Indels
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Pred. No. 2.6e+03;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                  Sequence 4, Application US/10027806
Publication No. US20020160476A1
GENERAL INFORMATION:
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Publication No. US20020198365A1
GENERAL INFORMATION:
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; Publication No. US20030054364A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Cenarchaeum symbiosum US-10-027-806-4
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FYPR: PRT
ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4
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Best Local Similarity 45.5%;
Matches 5; Conservative
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2294 EDVIPRGISFS 2304
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2294 EDVIPRGISFS 2304
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Best Local Similarity 45.5-
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2294 EDVIPRGISFS 2304
1 EEVVPXGMHYS 11
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US-10-027-801-4
                                                                                                                                   US-10-027-806-4
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Sequence 32076, Application US/10029386
| Publication No. US20030194704A1
| GRWERAL INFORMATION:
| APPLICANT: Penn, Sharron G.
| APPLICANT: Rank, David R.
| APPLICANT: Hanzel, David R.
| TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL POR TITLE OF INVENTION: BERPERSION ANALYSIS TWO FILE REFERENCE: AECMICA.X-2
| CURRENT APPLICATION NUMBER: US/10/029,386
| CURRENT APPLICATION DATE: 2001-12-20
| CURRENT RILING DATE: 2001-12-20
| NUMBER OF SEQ ID NOS: 34288
| SOFTWARE: Annowmax Sequence Listing Engine vere. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Board of Trustees of the University of Illinois
APPLICANT: Brimiano, Thomas
APPLICANT: Chang, Bey-dih
APPLICANT: Chang, Bey-dih
APPLICANT: Roninson, Igor
TILE OP INVENTION: Methods and Reagents for Identifying Gene Targets for Treating FILE REFERENCE: 99, 216-U
CURRENT FILING DATE: 2002-09-23
NUMBER OF SEQ ID NOS: 314
SOPTWARE: Patentin version 3.0
SEQ ID NO 241
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APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Robert A.
APPLICANT: Schlager, Christa
TITLE Schlager, Christa
FILE REFERENCE: DCORP.002A
CURRENT PELLOHONDER: US/10/027,801
CURRENT PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/408,020
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PSELSO for Windows Version 3.0
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                  7 DB 15;
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                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                        Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-10-199-820-241
Forumence 241, Application US/10199820
Forumence 241, Application US/10199820
GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-4
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60.0%;
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2294 EDVIPRGISFS 2304
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Best Local Similarity 60.0-
                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.9
Best Local Similarity 45.5
Matches 5; Conservative
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US-10-199-820-241
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US-10-116-275-114
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US-09-778-927A-53
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Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                     Score 32; DB 12; Length 236;
Pred. No. 2.3e+02;
1; Mismatches 2; Indels
                                                     PEATURE:

OTHER INFORMATION: MAP TO 298050.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.6

OTHER INFORMATION: EXPRESSED IN PRART, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: YOSHIYAWA, TSUTOMU
APPLICANT: OTSUTAM, MOTOYUKI
APPLICANT: OTSUTAM, MOTOYUKI
APPLICANT: MASUHO, YASHHKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR PILING DATE: 2002-01-24
PRIOR PILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2076, Application US/10094749
Publication No. US20030219741A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
ISHII, SHIZUKO
ISHII, SHIZUKO
ISONO, YUUKO
HIO, YURI
OTSUKA, KEBICHI
IRIB, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAMA, TSUTOMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.1%;
60.0%;
                                                                                                                                                                                                                                                                                   Query Match 57.1%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 3381
SOFTWARR: Patentin Ver. 2.1
SEQ ID NO 2076
LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EEVVPXGMHY 10
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                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMHYS 11
                                                                                                                                                                                                                                                                                                                                                                                                   80 VVPAGLTYS 88
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US-10-094-749-2076
                                                                                                                                                                                                                                               US-10-029-386-32076
   LENGTH: 236
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APPLICANT:
APPLICANT:
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RESULT 12

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Sequence 114, Application US/10116275
; Publication No. US20030211476A1
; Bublication No. US20030211476A1
; Bublication No. US20030211476A1
; GENERAL INPOWARTON:
; APPLICANT: Blan Pharmaceutical Technology
; APPLICANT: Brayden, David
; APPLICANT: Brayden, David
; APPLICANT: Brayden, David
; APPLICANT: LambKin, Imelda
; APPLICANT: LambKin, Imelda
; APPLICANT: LambKin, Lisa
; TITLB OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and
; TITLB OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; TURRENT APPLICATION UNMBER: US/10/116,275
; CURRENT APPLICATION UNMBER: US/10/116,275
; CURRENT PILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTMARE: PatchtIn version 3.1
; SEQ ID NO 114
; ELENTING
Sequence 53, Application US/09778927A

Sequence 53, Application US/09778927A

Patent No. USZO020068342A1

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL

TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING

TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING

FILE REFERENCE: 2786-01.60P

CURRENT APPLICATION NUMBER: US/09/778,927A

CURRENT PILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 81

SOFTWARE PATENTIN VET: 2.1

SEQ ID NO 53

LENGTH: 254
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Pred. No. 2.7e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.1%; Score 32; DB 9; Length 254; 60.0%; Pred. No. 2.5e+02; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRATURE:
INCATION: (1) - (1254)
OTHER INFORMATION: xaa = any amino acid, unknown, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 54, Application US/09919497; Patent No. US20020106662A1; GENBRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.1%;
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Matches 6; Conservative
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ORGANISM: Homo sapiens
US-10-116-275-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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Sequence 2, Application US/10024066

Publication No US20020166134A1

GENERAL INFORMATION:

APPLICANT: Field, Loren J.

APPLICANT: Field, Loren J.

TITLE OF INVENTION: CARDIOMYCCTES WITH ENHANCED PROLIFERATIVE POTENTIAL,

TITLE OF INVENTION: AND METHODS FOR PREPARING AND USING SAME

FILE REFERENCE: 7037-450

CURRENT APPLICATION NUMBER: US/10/024,066

FURENT FILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 2000-06-18

FRIOR FILING DATE: 2000-06-19

NUMBER OF SEQ ID NOS: 8

SOFTWARE PATENTIN VET. 2.1
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; APPLICANT: Mutter, George L.; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER; FILE REPERRORS: B0801/725
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR PRELICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PATENTIN VERSION 3.0
; SOFTWARE: PATENTIN VERSION 3.0
; SOFTWARE: PATENTIN VERSION 3.0
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-54
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Pred. No. 2.9e+02;
1; Mismatches 3; Indels
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Best Local Similarity 60.0%;
Matches 6; Conservative
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; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-024-066-2
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Search completed: December 22, 2003, 17:32:43 Job time: 21.9333 secs

73 EEVFPLAMIY 82

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

December 22, 2003, 17:24:36; Search time 9.06667 Seconds (without alignments) 116.675 Million cell updates/sec

US-09-909-164-11 56 1 BEVVPXGMHYS 11 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	ftsH proteinase ac	carbamoy1-phosphat	V1 protein - tobac				conserved hypothet	DNA binding protei	GMP synthetase, su	hypothetical prote	TSI8.1 protein - A	diphthine synthase	hypothetical prote	3-dehydroquinate s	probable DNA ligas	cell division prot	-	Slai protein precu		ATP-dependent DNA	hypothetical prote	polyamine transpor	conserved hypothet	probable amino aci	amino acid antipor	finger protein (cl	cytochrome-c3 hydr	coenzyme P420-quin	hypothetical nante
SUM	G	A72207	F89892	A42452	AE2001	\$69046	538143	D82618	T02590	H69194	T24111	G86430	G69117	C75538	B75478	T35025	E69086	C83903	\$58132	T28717	AF3286	854619	<b>B83607</b>	G82253	G71542	H81697	865811	HODVLB	A69284	T08564
	DB	2	~	~	~	~	~	N	N	~	~	N	N	N	~	N	~	~	~	N	ď	~	N	~	~	~	~	-	~	c
	Length	308	1057	102	252	460	743	156	233	311	425	510	264	279	350	355	360	425	426	495	1028	156	367	441	466	466	487	514	534	545
جن	Query Match	66.1	66.1	64.3	64.3	64.3	64.3	62.5	62.5	62.5	62.5	62.5	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	58.9		58.9	•	58.9	58.9	58.9	58.9	58.9
	Score	37	37	36	36	36	36	35	35	35	35	35	34	34	34	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33
	Result No.		7	m	4	Ŋ	Q	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

DNA mismatch repai	macrophage-stimula	C14B9.8 protein -	L-shaped tail fibe	hypothetical 367K	tachykinin B precu	heme_exporter_prot	hypothetical prote	ribosomal protein	ribosomal protein	probable Thua prot	hypothetical prote	cyclin D2 - rat	cyclin D2 - rat	cyclin D2 - mouse	cyclin D2 - human
A69663	JC5061	S44754	836851	T31308	A25905	D71640	S57810	E97120	T07215	C95881	T25737	JC4011	158372	A41984	A42822
~	-	7	ď	N	N	7	~	~	7	7	~	~	N	~	04
627	716	1257	1396	3472	126	197	225	233	267	270	283	288	288	289	289
58.9	58.9	58.9	58.9	58.9	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1
33	33	33	33	33	32	32	35	32	32	32	32	32	32	32	32
30	31	35	33	34	35	36	37	38	39	-04	41	42	43	44	45

# ALIGNMENTS

н	
RESULT	A72207

ftsH proteinase activity modulator HflK - Thermotoga maritima (strain MSB8)
C; Species: Thermotoga maritima
C; Species: 11.-Jun-1999 #sequence\_revision 11.-Jun-1999 #text\_change 21.-Jul-2000
C; Accession: A72207
R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hick Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, I

Nature 399, 323-329, 1999
A/Ittle: Evidence for lateral gene transfer between Archaea and Bacteria from genome s A/Ittle: Evidence for lateral gene transfer between Archaea and Bacteria from genome s A/Reference number: A72200; MUID:99287316; PMID:10360571
A/Status: preliminary
A/Accession: A72207
A/Accession: A72207
A/Accession: BNA
A/Accessio

C, Genetics

A;Gene: TM1822 C;Superfamily: erythrocyte band 7 integral membrane protein

Gaps 0 66.1%; Score 37; DB 2; Length 308; 75.0%; Pred. No. 10; 1; Mismatches 1; Indels Query Match Best Local Similarity 75.0° Matches 6, Conservative

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3 VVPXGMHY 10

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||| |:|| 41 VVPSGIHY 48

carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N3

Cispecies: Staphylococcus aureus
CiDate: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001
CiDate: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001
CiDate: 10-May-2001
Rixuxoda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-1057 - KUR>
A, Construction of the control of the c

A;Gene: pyrAB C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; bioti

Gaps

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AjExperimental source: strain 9a5c
Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as-Neco, R.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A;Authors: Perreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fro
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Lai
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.P.; Marino, C.L.; Marques, M.V.; Martins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein YBL011w homolog YKR067w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C;Accession: 538143
R;van Vliet-Reedijk, J.C.; Planta, R.J.
R;van Vliet-Reedijk, J.C.; Planta, R.J.
A;Accession: S38130
A;Accession: S38143
A;Molecule type: DNA
A;Residues: 1-743 < VANA
A;Residues: 1-743 < VANA
A;Cross-references: EMBL: Z28292; NID: 9486536; PIDN: CAA82146.1; PID: 9486537; MIPS: YKR06
A;Roperimental source: strain $288C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: D82618
R;Accession: D82618
A;Title: The Genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: D82618
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A;Molecule type: DNA
Residues: 1-156 <SIM>
A;Cross-references: GB:AE004014; GB:AE003849; NID:g9107044; PIDN:AAF84752.1; GSPDB:GNO
                             A;Accession: S69046
A;Molecule type: DNA
A;Residues: 1-460 <HAL>
A;Crossreferences: EMBL:U43703; NID:g1244769; PIDN:AAB68221.1; PID:g1244776; MIPS:YPL
C;Genetics:
                                                                                                                                                                                      A,Gene: SGD:UME1
A,CTOSE-references: SCD:S0006060; MIPS:YPL139c
A,Map position: 16L
C,Superfamily: Saccharomyces cerevisiae transcription modulator WTM1
                                                                                                                                                                                                                                                                                                                                           Query Match 64.3%; Score 36; DB 2; Length 460; Best Local Similarity 62.5%; Pred. No. 25; Matches 5; Conservative 2; Mismatches 1; Indels
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C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SGD:GPT2
A;Cross-references: SGD:S0001775
A, Reference number: S69040
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294 VVPCGLHY 301
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                            VI protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: 442452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
V;Tology 187, 633-642, 1992
A;Trie: The nucleotide sequence of the infectious cloned DNA component of tobacco yellc A;Reference number: 442452
A;Accession: 442452
A;Accession: 442452
A;Accession: Cycle (B)
A;Residues: 1-102 cMOR>
A;Residues: 1-102 cMOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
Nakase, S. 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A; Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
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C;Species: Nostoc sp. PCC 7120
S;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE2001
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A;Molecule type: DNA
A;Residues: .1-552 <KUR>
A;Coss-references: GB:BA000019; PIDN:BAB77929.1; PID:g17135383; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 17-Mar-2000
C;Accession: S69046
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                             Score 37; DB 2; Length 1057;
Pred. No. 39;
2; Mismatches 2; Indels
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                             66.1%;
60.0%;
   Ouery Match
Best Local Similarity 60...
6; Conservative
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7 QVVPSGINYS 16
                                                                                                                                                                  2 EVVPXGMHYS 11
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Best Local Similarity
Matches 6; Conserv
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S69046
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Gaps

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Gispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: Giskaio
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alone
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim,
C.A.; Li, Y.; Lin, X.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial
Rizzo, M.; Rocney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
A;Ttle: Sequence and analysis of chromosome, I of the plant Arabidopsis.
A;Accession: Giskaio
A;Accession: Giskaio
A;Accession: Giskaio
A;Accession: Giskaio
A;Residues: 1-510 <STO>
A;Residues: 1-510 <STO>
A;Cross-references: Gishacosinz; NID:g4587512; PIDN:AAD25743.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                      C;Accession: T24111

Submitted to the EMBL Data Library, October 1996
A;Reference number: Z19842
A;Accession: T24111
A;Accession: T24111
A;Status: pre-liminary, translated from GB/EMBL/DDBJ
A;Residus: 1-425
A;R
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C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Feb-2003
C; Accession: G69117
                                                                                                                                                                                                     hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct-1999
C;Accession: T24111
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60.0%; Pred. No. 45;
ive 2; Mismatches 2; Indels
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C,Superfamily: hexose phosphate transport protein uhpT
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A;Introns: 23/3; 56/3; 113/3; 257/2
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Best Local Similarity 60.0
Matches 6; Conservative
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        219 REVVESGLHES 229
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G86430
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C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Accession: H69194
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Ciu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-311 < MTH>
A;Residues: 1-311 < MTH>
A;Residues: 1-311 < MTH>
A;Experimental source: strain Delta H
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.P.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Numes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, A.M.; Silva, M.A.; da Silva, A.M.; Silva Jr., M.A.; da Silva, M.A.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Contents: annotation
C;Genetics:
A;Gene: XF1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Accession: T02590
R;Ohme-Takagi, M.; Shinshi, H.
Plant Cell.7, 173-182, 1995
A;Title: Ethylene-inducible DNA binding proteins that interact with an ethylene responsi
A;Reference number: Z14671; MUID:95276459; PMID:7756828
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C;Species: Nicotiana tabacum (common tobacco)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T02590
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Aolecule type: mRNA
A;Residues: 1-233 <0HM
A;Residues: 1-233 <0HM
A;Residues: 1-233 <0HM
A;Residues: 1-234 <0HM
A;Residues: EMBL:D38126; NID:g790362; PIDN:BAA07324.1; PID:g1208498
A;Rxperimental source: strain BY4; tissue-type leaf
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Pred. No. 19;
1; Mismatches 3; Indels
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Best Local Similarity 60...
Best Gonervative
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Matches 7; Conservative
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119 EEILPQGVH 127
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Best Local Similarity
Matches 5; Conserv
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A;Gene: MTH710
A;Start codon: GTG
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2; Indels

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Length 350;

DB 2;

3; Indels

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C;Species: Streptomyces collicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35025
R;Seegar, S; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Bubmitted to the EMBL Data Library, June 1999
A;Reference number: Z21565
A;Accession: T35025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <SEE>
A;Cross-references: EMBL:AL079355; PIDN:CAB45581.1; GSPDB:GN00070; SCOEDB:SC4C6.17c
A;Experimental source: strain A3(2)
C;Genetics:
A;Genetics:
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRO17: 1
A;Map position: 1
C;Superfamily: 3-dehydroquinate synthase; 3-dehydroquinate synthase homology
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Pred. No. 48;
1; Mismatches
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Best Local Similarity 60.0%;
Matches 6; Conservative
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S. Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-264 cMTH>
A;Residues: 1-264 cMTH>
A;Residues: 1-264 cMTH>
A;Residues: BNA
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: C7538
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ms.; Science 286, 1571-1577, 1999
S;Smith, H.O.; Venter, J.C.; Fraser, C.M.
A;Reference number: adjoresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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A;Molecule type: DNA
A;Residues: 1-279 <WHI>
A;Cross-references: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795
A;Experimental source: strain R1
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C;Species: Deinococcus radiodurans
C;Species: Data Deinococcus radiodurans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: B75478
R;White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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A,Map position: 1
C,Superfamily: Deinococcus radiodurans hypothetical protein DR0271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 264;
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A;Molecule type: DNA
A;Residues: 1-350 <WHI>
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Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 22, 2003, 16:43:51 ; Search time 4.6 Seconds Run on:

(without alignments) 112.455 Million cell updates/sec

US-09-909-164-11 56

1 EEVVPXGMHYS 11 Perfect score: Sequence:

**BLOSUM62** Scoring table: 127863 seqs, 47026705 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMADIES

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	d	Query Match		67.9	66.1	66.1	66.1	64.3	64.3	64.3	62.5	62.5	60.7	58.9	58.9	58.9	58.9	58.9	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	7	^	57.1	
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Q8936 buchnera ap P32784 saccharomyc O74377 schizosacch Q9kv29 vbbrio chol P15822 homo sapien P20273 homo sapien P7280 chimpanzee P97885 rattus norv Q58349 methanococc P10941 cryphonectr O28354 archaeoglob P52210 ovis aries
MOLB BUCBP SCT1 YRAST SULH-SCHPO REPC VIBCH ZEP1 HUMAN CD22 HUMAN CD22 HUMAN SYS SZO RAT Y339 METUA YHA1 CRYPA RL3 ARCFU
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578 759 877 1401 2717 847 130 276 319 331
2000 2000 2000 2000 2000 2000 2000 200
322 322 323 31.52 311 311
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# ALIGNMENTS

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REPURINGE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 25586;

MEDLINB-21886394; PubMed=11889109;

RA Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

RA Anderson I., Ivanova N., Grechkin G., Zhu L.,

RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman B., Bernal A.,

RA Larsen N., D'Souva M., Walunas T., Pusch G., Haselkorn R.,

RA Learen N., D'Souva M., Overbeek R.;

RA Learen N., D'Souva M., Overbeek R.;

RA Learen M., Kyrpides N., Overbeek R.;

RA Learen M., Kyrpides N., Overbeek R.;

RA Learen M., Kyrpides N., Overbeek R.;

RA Learen M., Ryrpides N., Overbeek R.;

RA Learen M., Ryrpides N., Overbeek R.;

RA Learen M., Ryrpides V., Overbeek R.;

RA Learen M., Ryrpides N., Overbeek R.;

RA Learen M., Ryridis M., Ryrpides N., Mich Respective Remin Ly.
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                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
phosphate synthase large chain (RC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CARB OR FN0422.
                                                                                                                                                                                                                                                                     Pusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria, Fusobacterales, Fusobacteriaceae,
                                                        PRT; 1058 AA
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InterPro; IPR006275; CarA_L glu.
InterPro; IPR005483; CPase_L.
InterPro; IPR005480; CPase_L.D2.
InterPro; IPR005480; CPase_L.D3.
InterPro; IPR005481; CPase_L.N.
InterPro; IPR004362; MGS IIke.
Pfam; PP00289; CPSase_L.Chain; 2.
Pfam; PP02786; CPSase_L.D2; 2.
Pfam; PP02787; CPSase_L.D3; 1.
                                                        STANDARD;
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CARB_FUSNN
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Matches
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MBDLINE=22508454; PubMed=12620739;
MAKIND K., Obhima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Ijjima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
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distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (BC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (RPSPS)
AROA OR VP1020.
                                                                                                                                                                OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                               ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
AMANGANESE 1 (BY SIMILARITY).
AMANGANESE 2 (BY SIMILARITY).
AMANGANESE 3 (BY SIMILARITY).
                           PRINTS, FRUNCHOST, CESABELI LTG; 1.

PROSITE; PS00866; CPSASE 1; 2.

PROSITE; PS00867; CPSASE 2; 2.

Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

ATP-binding; Manganese; Complete protecome.

DOMAIN

1 401

CARROXYPROSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 1; Length 1058; Pred. No. 10; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBUNIT: Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-1- SIMILARITY: Belongs to the EPSP synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP005076; BAC59283.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|| |::||
190 EIVPNGLNYS 199
                       PRINTS; PR00098; CPSASE
                                                                                                                                               401
546
929
1058
546
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Pfam; PF02142; MGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00210; -; 1
                                                                                                                                                                                                                                                                   153 21
302 35
284 28
298 29
300 82
820 82
1058 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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Q87QX9;
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REPEAT
NP_BIND
NP_BIND
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DOMAIN
DOMAIN
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AROA_VIBPA
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Matches
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-I- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + popphate + L-glutamate + carbamoyl phosphate.

-I- COPACTOR: Binds 3 manganese ions per subunit (By similarity).

-I- PATHWAY: Arginine biosynthesis.

-I- PATHWAY: Arginine biosynthesis, first step.

-I- RATHWAY: Composed of two chains, the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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STRAIN=MISO, ARCC 700699, and N315;
MEDLINB=21311952; PubMed=11418146;
MEDLINB=21311952; PubMed=11418146;
MIDLINB=21311952; PubMed=11418146;
MIN Construction of the co
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28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (RC 6.3.5.5) (Carbamoyl-phosphate synthase large chain (RC 6.3.5.5) (Carbamoyl-phosphate synthase ammonia chain).
CARB OR PYRAB OR SAV1203 OR SA1046.
Staphylococcus aureus (strain Mu35) / ATCC 700699), and Staphylococcus aureus (strain Mu35).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
PROSITE; PSO0104; EPSP_SYNTHASE_1; 1.
PROSITE; PS00885; ERSP_SYNTHASE_2; 1.
Aromatic amino acid blosynthesis; Transferase; Complete proteome.
SEQUENCE 426 AA; 46094 MW; 373D39CCSBA1F70F CRC64;
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                                                                                                                                                                                                                                                                       Score 37; DB 1; Length 426;
Pred. No. 6.3;
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                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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EMBL; AP003132; BAB42298.1; -.
HSSP; P00968; LCSO.
HAWAP; MF 01210; -; 1.
InterPro; IPR00545; CARA L glu.
InterPro; IPR005483; CPase L.
InterPro; IPR005483; CPase L.
InterPro; IPR005481; CPase L.
InterPro; IPR005481; CPase L.
InterPro; IPR005481; CPase L.
InterPro; IPR005481; CPase L.D3.
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60.0%;
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Best Local Similarity
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ID CARB STAAM
AC Q99UR5;
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OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                           Arginine blosynthesis; Primidine blosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete proteome.

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1; Length 1057; Pred. No. 16;
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Last annotation update)
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TIGRARMS; TIGRO1369; CPSASEII_lrg; 1.
PROSITE; PRO0866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE_2; 2.
                                                                              InterPro; IPR005483; CPase L. D. InterPro; IPR005493; CPase L. D2. InterPro; IPR005480; CPase L. D3. InterPro; IPR005480; CPase L. D3. InterPro; IPR005481; CPase L. D3. InterPro; IPR005481; CPase L. D3. Pfam; PF002786; CPase L. Chain; 2. Pfam; PF02786; CPase L. LD2; 2. Pfam; PF02787; CPSase L. D3; 1.
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                                           HAMAP; MP_01210; -; 1.
InterPro; IPR006275; CarA_L_glu.
                            AP004825; BAB94951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-OCT-1993 (Rel. 27, Last ann
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.1%;
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1057
546
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ID YIIK TYDVA
P31619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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DOMAIN
DOMAIN
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NP BIND
NP BIND
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R Pfam; PF02787; CPSase L D3; 1.

R Pfam; PF02185; CPSase L D3; 1.

R R Pfam; PF00109; CPSASE L D3; 1.

R R ROSITE; PS00866; CPSASE 1; 2.

R R ROSITE; PS00867; CPSASE 1; 2.

R R ROSITE; PS00867; CPSASE 1; 2.

R Arginine biosynthesis; Primidine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Ligase; Repeat; Arginine biosynthesis; Ligase; Repeat; DOMAIN 1 401 CARBOXPHOSPHATE SYNTHETIC DOMAIN.

I DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

I DOMAIN 930 1057 ALLOSTERIC DOMAIN.
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MEDLINE=22040717; PubMed=12044378;

MEDLINE=22040717; PubMed=12044378;

Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagan T., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamanto K., Hiramatan K.;

"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
phosphate synthetes annonia chain (EC 6.3.5.5) (Carbamoyl-CARB OR PYRAB OR MW1086.
                                                                                                                                                                                                                                                                                                                                             MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.1%; Score 37; DB 1; Length 1057; 60.0%; Pred. No. 16; 2; Indels Live 2; Mismatches 2; Indels
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Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              117171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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153 21
302 35
284 28
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820 82
832 83
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P58940;
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SEQUENCE
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Matches
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        DARAGE STATE OF THE SOLUTION O
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Gaps

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2; Indels

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                                                                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                         Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
"The nucleotide sequence of the infectious cloned DNA component tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotylednous plants.";
Virology 187:633-642(1992).
Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
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RESULT 7
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XY MEDLINE=97313-71; PubMed=9169875;

XY BUSSEY H., Storms R.K., Ahmed A., Albermann K., Allen B., Ansorge W., Bussey H., Storms R.K., Ahmed A., Albermann K., Benes V., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Araujo R., Aparicio A., Burcher M., Carpenter J., Cherry J.M., Abotstein D., Bowman S., Buckner M., Chung E., Churcher C.M., Coster F., Davis R.W., Chung E., Churcher C.M., Coster F., Davis R.W., Abelius H., Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U., Heumann K., Hilbert H., Hillier L., Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., A Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis B.J., Marathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D., Amathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D., Amaler P., Pearson D., Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Schramm S., Schramm S., Schraeder M., Sdicu A.M., Tettelin H., Winnett B., And M. A., No D.H., Hani J., Wedler H., Winnett B., And M. A., Vo D.H., Hani J., Malsh S.V., Amblut R., Waller S., Woosh H., Hani J., Hani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: TRANSCRIPTIONAL MODULATOR WITH ROLES IN MEIOTIC REGULATION AND SILENCING, NEGATIVE REGULATOR OF MEIOSIS.
-1- SIMILARITY: CONTAINS 4 WD repeats.
-1- SIMILARITY: STRONG, TO YEAST WIMI AND WIM2.
                                                                                                         Score 36; DB 1; Length 102; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mallory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                 InterPro, IPR002621, Gemini mov.
Pfam, PR01708, Gemini mov.
Hypothetical protein.
SEQUENCE 102 AA, 11178 MW, A40ECFIEOAF55B67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           , Last sequence update)
                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Meiosis negative regulator UME1. UME1 OR WTM3 OR YPL139C OR LP17C.
                                                                                                                                                                                                                                                                                                                UMEI_YEAST STANDARD, 1003010; P87330; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence 1895-2003 (Rel. 41, Last annotation)
                                                                                                           64.3%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U10280; AAB40937.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U43703; AAB68221.1; -. PIR; S69046; S69046.
TRANSFAC; T04309; -. SGD; S0006060; UME1.
                                                                                                                             Local Similarity 60.0 tes 6; Conservative
                                                                                                                                                                                                           2 EVVPXGMHYS 11
PIR; A42452; A42452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A364A;
                                                                                                               Query Match
                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO, GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0004366; F:glycerol---phosphate O-acyltransferase acti. . .; IDA.
GO; GO:0008654; P:phospholipid biosynthesis; IDA.
InterPro; IPRO2123; Acyltransferase.
Ffam; PF01553; Acyltransferase; 1.
SWART; SW00563; PlsC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Pungi, Ascomycota; Saccharomycotina, Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              van Vilet-Reedijk J.C., Planta R.J.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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01-ZUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCP1-MET1 intergenic region.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0003714; F:transcription co-repressor activity; IDA.
GO:0040020; P:transcription of meiosis; IGI.
InterPro; IPRO0180; WD40.
Ffam; PF00400; WD40; 3.
SWART; SW00320; WD40; 4.
PROSITE; PS50082; WD REPEATS 1; FALSE NEG.
PROSITE; PS50082; WD REPEATS 2; FALSE NEG.
PROSITE; PS50082; WD REPEATS REGION; FALSE NEG.
PROSITE; PS50084; WD REPEATS REGION; FALSE NEG.
PROSITE; PS50084; WD REPEATS REGION; FALSE NEG.
PREPEAT 233 271 MD 1.
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 460;
Pred. No. 11;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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539 555 POTENTIAL.
743 AA; 83644 MW; 84B9946E56B62F15 CRC64;
                                                                                                                                                                                                                                                                                                                                                    AA6F60448B7BCBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    743 AA.
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Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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                                                                                                                                                                                                                                                                                                      各各
                                                                                                                                                                                                                                                                                                                                                       51022 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                        64.3%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 62.5
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                       460 AA;
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SGD; S0001775; GPT2.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                              276
339
411
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ID YK47 YEAST
AC P36148;
                                                                                                                                                                                                                                                                                                                               REPEAT
SEQUENCE
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SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                      RX MEDLINE-Delta H;

RX MEDLINE-Delta H;

RX MEDLINE-Delta H;

RA Aldredge T., Daucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,

RA Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K.,

RA Aldredge T., Bashizzadeh R., Palakely D., Cook R., Gilbort K.,

RA Aldredge T., Bashizzadeh R., Palakely D., Cook R., Gilbon R.,

RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

RA Daniels C.J., Mao J.-II, Rice P., Noelling J., Reeve J.N.;

RY "Complete genome sequence of Methanobacterium thermoautctrophicum

RT deltaH: functional analysis and comparative genomics.";

L. Bacteriol. 1797-1735-7155 (1997).

C. - CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine +

H(2)O = AMP + diphosphate + GMP + L-glutamate.

C. - ATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine +

H(2)O = AMP + diphosphate + GMP + L-glutamate.

C. - SUBUNIT: HETERODIMER COMPOSED OR A GLUTAMINE ANIDOTRANSFERASE

C. - SUBUNIT: HETERODIMER COMPOSED OR A GLUTAMINE ANIDOTRANSFERASE

C. - SUBUNIT: AND A GMP SYNTHASE SUBUNIT (B) (POTENTIAL).

C. - SIMILARITY: BELONG TO THE GMP SYNTHASE PAMILY.
                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (BC 6.3.5.2) (GMP
                                                                                                                                                                                      GÜAAB OR WIH710.
Methanobacterium thermoautotrophicum.
Archaea, Buryarchaeota; Methanobacteria; Methanobacteriaceas;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MP_00345; -; 1.
InterPro; IPR001674; GMP synt_C.
Emm; PR00958; GMP synt_C.
TIGRPAMs; TIGR0084; guaA. Cterm; 1.
Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.5%; Score 35; DB 1; Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 184 GMP-BINDING (BY SIMILARITY).
29 35 ATP (BY SIMILARITY).
308 AA; 34403 MW; P2DCP6ED202CAECI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YARLI SIMULE SIM
   308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000850; AAB85215.1; ALT_INIT.
   PRT;
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Matches 7; Conservative
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 KEVVESGLHES 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P04079; 1GPM.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE PROM N.A.
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Complete proteome.
GAAB METTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1sopentenyl-diphosphate delta-isomerase 1 (EC 5.3.3.2) (IPP isomerase
1) (Isopentenyl pyrophosphate isomerase 1) (IPP11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY.
-!- PATHWAY: ISOPRENOID BIOSYNTHETIC PATHWAY WHOSE END PRODUCTS
INCLUDE DOLICHOLS, VITAMINS A, D, E, AND K, STEROID HORMONES,
CAROTENOIDS BILE ACIDS AND CHOLESTEROL.
-!- SUBCELLULAR LOCATION: Peroxisomal.
-!- SIMILARITY: Belongs to the IPP isomerase type 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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148 BY SIMILARITY.
8 SIMILARITY.
26317 MY. P500A6586385E803 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholesterol biosynthesis,
                                                                                                                                                                                                                                         227 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesocricetus auratus (Golden hamster).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom, PD004109, IPP isomerase; 1. Carotenoid biosynthesIs; Cholestero
                                                                                                                                                                                                                                      IDII_MESAU STANDARD; E 035586; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequis-SEP-2003 (Rel. 42, Last anno
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294 VVPCGLHY 301
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3; Indele

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNID. Unstratute the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-JAN-1990 (Rel. 13, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Periplasmic [NiFeSe] hydrogenase large subunit (RC 1.12.99.6) (NiFeSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
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Besulfowiczobium baculatus).
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfowibrionales;
Desulfomicrobiaceae; Desulfomicrobium.
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                              -i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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2; Mismatches
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Bacteriol. 176:4219-4225(1994)
                                                                                                                                                                                                                                                                                                                                              EMBL; AP005080; BAC60378.1; -. EMBL; U06949; AAA21571.1; -.
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Best Local Similarity
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P13065;
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                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 20460 / W29;

X MEDLINE=96216076; PubMed=8662639;

Boistame A., Beckerich J.-M., Gaillardin C.;

Boistame A., Beckerich J.-M., Gaillardin C.;

"Sl81p, an endoplasmic reticulum component, is involved in the protein translocation process in the yeast Yarrowia lipolytica.";

J. Biol. Chem. 271:11668-11675(1996).

"INTERACT DIRECTLY WITH TRANSLOCATING POLYPEPTIDES TO FACILITATE TRANSFER AND/OR HELP THEIR FOLDING IN THE ER. IT IS NOT REQUIRED FOR VIABILITY BUT IS ESSENTIAL FOR OPTIMAL GROWTH AT ELEVATED TEMPERATURES.

"INTERACT TEMPERATURES.

"ELEVATED TEMPERATURES.

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MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEST PROTEIN.
PREVENT SECRETION PROM ER (POTENTIAL)
, 0ACD/2E117540B8E2 CRC64;
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Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.7%; Score 34; DB 1; Length 426; 44.4%; Pred. No. 26;
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15-SPP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical protein VP2115 (ORF3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 AA
      Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z50154; CAA90516.1; -.
PIR; S58132; S58132.
InterPro; IPR000886; ER target.
PROSITE; PS00014; ER TARGET; 1.
Endoplasmic reticulum; Signal.
SIGNAL 1 17 POTE
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52 DQVIPAGLH 60
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Best Local Similarity
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                                 NCBI_TaxID=4952;
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WEDLINE=96349107; PubMed=8760914;
MEDLINE=96349107; PubMed=8760914;
Ganeti R., Perego M., Albertini A.M., Galizzi A.;
Bacillus aubtilis mutb operon: identification, nucleotide sequence and mutageneeis.m;
Microbiology 142:2021-2029(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.9%; Score 33; DB 1; Length 513; 71.4%; Pred. No. 50; 1; Mismatches 1; Indels ive
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01-077-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
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  297 PGGLHYS 303
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493 4
513 AA;
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Bacillus subtilis.
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SEQUENCE FROM N.A.
  RESULT 13
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                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            | Remain | R
                                                                                                       ø
                                            ligands.
SUBUNIT: Heterodimer of a large and a small subunit.
SUBCELLULAR LOCATION: Periplasmic.
MISCELLANBOUS: PERHAPS THE LEADER OF THE SMALL SUBUNIT SERVES AS
THANSPORT VEHICLE FOR BOTH SUBUNITS.
SIMILARITY: BELONGS TO THE [NIFE]/[NIFESE] HYDROGENASE LARGE
SUBUNIT FAMILY.
COFACTOR: Nickel, 2 irons and selenocysteine. Iron 1 has three cyanide and carbon monoxide ligands. Iron 2 has three water
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ligands
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Gaps

PRT; 1188 AA.

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                                       RA Kunst F. Ogsamwara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Rarington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G. Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Mizuno M., Moeelt D., Nakai S., Nubako K.,
RA Kobayashi Y., Koetter P., Mizuno M., Moeelt D., Nakai S., Nubako K.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
RA Redorn M., Rivolta C., Rocha B., Roche B., Roy M., Sato T.,
RA Sato T., Scanlan B., Schoels B., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan B., Schoels B., Roche B., Tosenout A.,
RA Schiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi H., Tarahashi H., Taremaru K.,
RA Vasidua K., Yoshikawa H.F., Zumstein B., Yoshikawa H., Danchin A.,
The complete genome sequence of the Gram-positive bacterium Bacillus
RT "The complete genome sequence of the Gram-positive was and the sequence of the Gram-positive medical sequence and the gram-positive was and the sequence of the care of the sequence was and the sequence of the sequence of the sequence was and the sequence was and the sequence of the
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-! FUNCTION: THIS RECOTEIN IS INVOLVED IN THE REPAIR OF MISMATCHES IN DNA. IT IS REQUIRED FOR DAM-DEPENDENT METHYL-DIRECTED DNA MISMATCH REPAIR. MAY ACT AS A "MOLECULAR MATCHANKER", A PROTEIN THAT PROMOTES THE FORMATION OF A STABLE COMPLEX BETWEEN TWO OR MORE DNA-BINDING PROTEINS IN AN ATP-DEPENDENT MANNER WITHOUT ITSELF BEING PART OF A FINAL REFECTOR COMPLEX (BY SIMILARITY).

-! SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.9%; Score 33; DB 1; Length 627; 54.5%; Pred. No. 62; ive 1; Mismatches 4; Indels
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DNA repair; Complete protecme.
SEQUENCE 627 AA; 70431 MW; 068A0509CC265
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HAVAP; MF 00149; -; 1.
InterPro; IPR001559; ATPbind ATPase.
InterPro; IPR002099; DNA_mis_repair.
Pfam; PF01119; DNA_mis_repair; 1.
Pfam; PF01119; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
                               MEDLINE=98044033; PubMed=9384377;
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HSSP; P23367; 1BKN.
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                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable phosphorylase B kinase alpha regulatory chain (Phosphorylase
kinase alpha subunit).
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                                                                                          Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                     "2.2 Mb of contiguous nucleotide sequence from chromosome III of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein, Glycogen metabolism, Calmodulin-binding.
SEQUENCE 1188 AA; 135558 MW; DE9BBB75F3603863 CRC64;
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VLTF BETS

AC P1330; O48502;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-MAY-2006 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L15188; AAA27954.2; -.
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hes 6; Conservative
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                                                                                Caenorhabditis elegans.
                                                                                                                                              SEQUENCE FROM N.A.
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DB L-baped tail fiber protein (LTF protein).

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Search completed: December 22, 2003, 17:42:26 Job time : 4.6 secs

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Q8cpj4 staphylococ
Q9kx22 thermocpas
Q9k1h8 thermoplasm
Q8d1h0 synechococ
Q46486 corynebacte
Q8ywp1 anabaena sp
Q8ywp1 anabaena sp
Q8ywp1 nicotiana ta
Q9pc35 xylella fas
Q9pc35 xylella fas
Q9yw50 nicotiana t
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Q9w60 nicotiana t
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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1: sp archea:*
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08C2B4
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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Maximum DB seq length: 200000000
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Match Length DB
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1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	; 22, C 22, L 23, L guence rdata; entia;	the the character of th	, 23, 23, 13, thas
22 22 22 23 25 25 25 25 25 25 25 25 25 25 25 25 25	MINARY; Birel. 22, Ci Birel. 23, Li Birel. 23, Li Bed sequence se).	rg R.; rg R.; d (JUN-2002) to d (JUN-20195; AAH12195; 1915724; 1110006; 413 AA; 4662 is similarity 63. 7; Conservative BEVVPXGMHYS 11	PRELIMINARY; (TrEMBLrel. 23, ( TrEMBLrel. 23, I (TrEMBLrel. 23, I
CCCCCCCCCCCCCCC	ELII FERM FERM MOU FESO FESO 90;	N.A. 24; A.A. AA. AA. AA. KGM	SLII CEM CEM CEM
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STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamotc Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakaraki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1."; DNA Res. 9:123-130(2002).

EMBL, AP005374; BAC09170.1; -. Complete protecome.

SEQUENCE 1044 AA; 113205 MW; 0089C13F0F636D2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.1%; Score 37; DB 16; Length 1044; 63.6%; Pred. No. 98; 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.1%; Score 37; DB 17; Length 322; 75.0%; Pred. No. 27; ive 1; Mismatches 1; Indels
              Thermoplasma acidophilum.
Archaes, Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataccae; Thermoplasma.
YGEL_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elongatus).
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Bacteria, Cyanobacteria, Chroococcales, Synechococcus.
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Last annotation update)
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(TrEMBLrel. 23, Last annotation update)
Glucose-fructose oxidoreductase related protein
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MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                                                                                                                                           Nature 407:508-513(2000).
EMBL, ALG45063, CAC11395.1; -.
Interpro, IPR000683, GFO_IDH_MCA.
Pfam, PF01408; GFO_IDH_MCA, 1.
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01-MAR-2003 (TrEMBLrel. 23, Le
Multidrug efflux transporter.
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                          SEQUENCE PROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome
SEQUENCE 322 AA
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01-NOV-1996
01-MAR-2001
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Q8DIH0;
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STRAIN=MSB8 / DSM 3109;
STRAIN=MSB8 / DSM 3109;
MEDLINE=99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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                                                                                                                                     STRAIN-ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y.,
Chen Z., Wen Y.,
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016746; AA004476.1; -.
                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 16; Length 1057;
Pred. No. 38;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 1057 AA; 117391 MW; 8944D7D8DB1CAE59 CRC64;
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SEQUENCE 308 Aa; 34778 MW; ADE03603E5101A9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9X2E2;
01-NVV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
11-NAR-2003 (TrEMBLrel. 23, Last annotation update)
FTSH protease activity modulator HFLK.
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Last annotation update)
Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band 7; 1.
PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
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Best Local Similarity 63.6%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                             SEQUENCE FROM N.A.
                                                        NCBI_TaxID=1282;
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. Alaska;
MEDLINE-21231727; PubMed-11333309;
Sassa N., Matsushita Y., Nakamura T., Nyunoya H.;
"The Molecular Characterization and in situ Expression Pattern of Pea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-96020672; PubMed=7476204;
Moses B.K., Good R.T., Sinistaj M., Billington S.J., Langford C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-9627263, PubMed-8654969;
MEDLINE-9627263, PubMed-8654969;
Billington 8.J., Sinistaj M., Cheetham B.F., Ayres A., Moses E.K.,
Katz M.E., Rood J.I.;
"Identification of a native Dichelobacter nodosus plasmid and
implications for the evolution of the vap regions.";
EMBL; U02462; AAB12366.1; -
InterPro, IRR001837; BRCT.
EMBL; PR00531; BRCT; 1.
SMART; SM00292; BRCT; 1.
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Bacteria, Proteobacteria, Gammaproteobacteria, Cardiobacteriales,
Cardiobacteriaceae, Dichelobacter.
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45.5%; Pred. No. 1.2e+02;
ive 4; Mismatches 2; Indels
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InterPro; IPR001444; Flag_bb_rod.
InterPro; IPR0015202; GRAS.
InterPro; IPR005202; GRAS.
Pfam; PP03154; GRAS; 1.
PROSITE; PS00588; FLAGELIA BB ROD; 1.
SEQUENCE 819 AA; 90372 MW; 41B67BD6DC72ADFA CRC64;
                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                 819 AA
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                                                                                                                                                    PRT;
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(TrEMBLrel. 17, L
(TrEMBLrel. 23, L
                                                                                                                                                                                                                                                                                                                                                      Pisum sativum (Garden pea).
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Query Match
Best Local Similarity 45.5%;
Bertanive
5; Conservative
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      EMIVPAGLHP 244
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01-JUN-2001 (
01-JUN-2001 (
01-MAR-2003 (
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         235
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Q57489;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=C.striatum; STRAIN=M82B;
MEDLINE=20194806; PubMed=10732668;
Tauch A., Krieft S., Kalinowski J., Puhler A.;
The 51,409-bp R-plasmid pTPIO from the multiresistant clinical isolate Corynebacterium striatum M82B is composed of DNA segments initially identified in soil bacteria and in plant, animal, and human
                                                                                                                                                                                                                                                        SPECIES=C.xerosis; STRAIN=W82B; MEDLINE=96117603; PubMed=8559800; Tauch A., Kassing F., Kalinowski J., Puhler A.; Tauch A., Kassing F., Kalinowski J., Puhler A.; The Corynebacterium xerosis composite transposon Tn5432 consists of two identical insertion sequences, designated IS1249, flanking the erythromycin resistance gene ermCX."; Plasmid 34:119-131(1995).
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MEDLINE=21555285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Ratenabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
"Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
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                                                                                       Corynebacterium striatum.
Bacteria, Actinobacteridae, Actinomycetales,
Corynebacterinaes, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1725, 43770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.3%; Score 36; DB 2; Length 208; 50.0%; Pred. No. 27; ive 3; Mismatches 2; Indele
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EMBL; U21300; AAC95478.1; -.

EMBL; AF024666, AAG9390.1; -.

Hypothetical protein; Plasmid.

SEQUENCE 208 AA; 23012 MW; PIS04BEIECDE85A6 CRC64;
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EMBL, AP001586; BAB77929.1; -
HYPOCHETICAL protein; Complete proteome.

SEQUENCE 252 AA; 28831 NW; 925572DASDICA519 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBYWP1;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Alr1563.
Hypothetical 23.0 kDa protein (GcrA)
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                                                            Corynebacterium xerosis, and
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Matches 5; Conserv
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Q8YWP1

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RESULT 7 Q8YWP:

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Length 819;

of Omp1

233 AA.

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PRELIMINARY;
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STRAINN=2055717; PubMed=10910347;
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Agcencio M.,
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Baptiste C.S.,
Barros M.H., Bonaccorei B.D., Bordin S., Bove J.M., Briones M.R.S.,
Barros M.H., Bonaccorei B.D., Bordin S., Bove J.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Carrer D.M.,
Colutinho L.L., Cristofani M., Dias.Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Raraga J.S., Franca S.C., Franco M.C., Frohme M., Fullan L.R.,
Radanier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
Racieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.P., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B., Martins E.M.F., Martino C.L.,
Machado M.A., Madeira A.M.B., Martins E.M.F., Matsukuma A.Y.,
Machado M.A., Madeira A.M.B., Martins E.M.F., Matsukuma A.Y.,
Manni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Oliveira M.C., de Oliveira R.C., Painleir D.M., Pairs A.,
RA Goliveira M.C., de Oliveira R.C., Painleir D.M., Pairs A.,
RA de Rosea V.B. Jr., Martins B.M., da Silva M.A.,
RA da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.P., Terenzi M.R., Teuhako M.H.,
RA Zago M.A., Zatz M., Meidania J.C.;
Natura And., St. Terenzi M.R., Meidania S., Vettore A.L.,
RThe genome sequence of the plant pathogen Xylella fastidiosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
11 TaxID=2371;
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                                                                                                                       Length 139;
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SEQUENCE 156 AA; 17144 MW; D8358619C6671ASD CRC64;
                                                  1
139 AA; 15052 MW; BOBIIOAA4B7D4708 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0c7-2000 (TrEMBLrel. 15, Created)
01-0c7-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein Xf1950.
                                                                                                                         62.5%; Score 35; DB 2; 55.6%; Pred. No. 28;
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EMBL; AE004014; AAF84752.1; -.
PROSITE; PS50172; BRCT; 1.
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EEILPQGVH 127
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21 IVPAGVHWS 29
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SEQUENCE
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                       Ligase.
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Matches
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                                                                                                  Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamida; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana sylvestris (Wood tobacco).

Makaryota, Viridiplantae; Streptophyta, Pmbryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Asteridae, lamiids; Solanales; Solanacese, Nicotiana.
                                                                                                                                                                                             SECUENCE FROM N.A.

STRAIN=BY4; TISSUB=Leaf;
MEDLINE=95276459; PubMed=7756828;
Ohme-Takagi M., Shinshi H.;
"Ethylene-inducible DNA binding proteins that interact with an ethylene responsive element.";
Plant Cell 7:173-182(1995).
EMBL; D38126; BAA77324.1; -.
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SEQUENCE 237 AA; 26243 MW; 01BC3EBB51E46298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25563 MW; 6CD16783582C0CB5 CRC64;
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Last annotation update)
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Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence u
01-WAR-2003 (TrEMBLrel. 23, Last annotation
Bthylene-responsive element binding factor.
    Created)
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                                                                              Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T02654; -.
InterPro; IPR001471; TP ERF.
Prom; PP00847; AP2-domaTn; 1.
SMART; SM00380; AP2; 1.
                    01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23,
(TrEMBLrel. 01,
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Best Local Similarity 60.0%,
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Best Local Similarity 60.0
Matches 6; Conservative
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94 QAVVPKGRHY 103

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MEDIINE=93231538; PubMed=8472961; Fremaux C., De Antoni G., Raya R., Klaenhammer T.; "Genetic organization and sequence of the region encoding integrative functions from Lactobacillus gasseri temperate bacteriophage phi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Engel G., Altermann B., Klein J., Henrich B.;
"Structure of a genome region of the Lactobacillus gasseri temperate phage phi adh covering a repressor gene and cognate promoters.";
Gene 210:67-70(1998).
EMBL; AJ11519; CAB52540.1; -.
InterPro; IPR002053; Glyco_hydro_25.
InterPro; IPR003646; SH3 bac.
Pfam; PF01183; Glyco_hydro_25; 1.
Probom; PD004620; Glyco_hydro_25; 1.
Probom; PD004620; Glyco_hydro_25; 1.
SMART; SM00641; Glyco_hydro_25; 1.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99384014; PubMed=10452853;
Altermann E., Klain J., Henrich B.;
Altermann E., Klain J., Henrich B.;
"Primary structure and features of the genome of the Lactobacillus gasseri temperate bacteriophage phi-adh.";
                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI TaxID=12417;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=95138034; PubMed=7836307;
Henrich B., Binishofer B., Blaesly U.;
Primary structure and functional analysis of the lysis genes of
Lactobacillus gasseri bacteriophage phi-adh.";
J. Bacteriol. 177:723-732(1995).
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                                                                                                                                                                                                                     Altermann B.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 AA; 34703 MW; 9FF2715EE43561C7 CRC64;
                                                            Created)
Last sequence update)
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                                                            01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23,
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                                 PRELIMINARY;
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Q9XVK4;
01-NOV-1999 (
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RESULT 13
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Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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R10D12.10.
Caenorhabditis elegans.
Bukaryota, Metazoa; Nematoda; Chromadorea, Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu & Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu & Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A., Altafi i Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M., Abare I.R., Federapial N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC TSIS sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                        'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                  62.5%; Score 35; DB 5; Length 425; 50.0%; Pred. No. 95; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                              Percy C.M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Transferase.
SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 AA
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Solince 282:2012-2018(1998).
Solince 282:2012-2018(1998).
SCHENCE 28110; CAB03241.1; -.
WormPep; R10D12.10; CR12690.
InterPro; IPR000719; Prot_Kinase.
Pfam; PP000069; pkinase; 1.
Probom; PD000001; Prot_Kinase; 1.
PROSITS; PS50011; PROTEIN_KINASE_DOM; 1.
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                                                                                                                                                                         MEDLINE=99069613; PubMed=9851916;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAK-2003 (TrEMBLrel. 23,
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Best Local Similarity 50.0%;
S; Conservative
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PROSITE; PS50850; MFS; 1.
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Best Local Similarity
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                                                                                             SEQUENCE FROM N.A.
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                                                           NCBI_TaxID=6239;
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Search completed: December 22, 2003, 17:51:29

Job time : 25.2667 secs

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sequence 10, Appl
Sequence 11, Appl
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Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 21, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 8, Appli
Sequence 6, Appli
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                                                                     ; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
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1: /cgn2 6/ptodate/1/laa/5A COMB.pep:*
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3: /cgn2 6/ptodate/1/laa/6A_COMB.pep:*
4: /cgn2 6/ptodate/1/laa/6A_COMB.pep:*
5: /cgn2 6/ptodate/1/laa/6B_COMB.pep:*
6: /cgn2 6/ptodate/1/laa/backfles1.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-394-272-10

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US-09-051-341-7

US-09-394-272-8

US-09-394-272-4

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US-08-569-147-82

US-08-569-147-82

US-08-569-147-82

US-08-953-91A-31637

US-09-252-991A-31637

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US-08-963-851-14

US-09-819-989-4
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                                                                                                                                                                                                           328717 seqs, 42310858 residues
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                                                                     December 22, 2003, 16:37:03
                                              OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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PERMITANT INFORMATION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: SUCROSE PROPERTY APPLICATION NUMBER: US/08/853,948B

CURRENT PILLING DATE: 197-05-09

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PATENTING DATE: 100

SOFTWARE: PATENTING DATE: 1341

TYPE: FRT

ORGANISM: Citrus unshiu

FRANTUR:

OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg, Asn, Asp,

OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe,

16-08-853-948B-4
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Patent No. 6210943
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
THE REPRESENCE:
TITLE OF INVENTION:
THE REPRESENCE:
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Pred. No. 18;
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                                                US-08-246-361A-21

US-08-246-361A-21

US-08-246-361A-21

US-08-26-842B-20

US-08-246-361A-22

US-08-463-772-22

US-08-463-772-22

US-08-463-772-22

US-08-464-51A-4172

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US-08-464-517-23
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TYPE: PRT; ORGANISM: Citrus unshiu US-08-853-948B-5
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Best Local Similarity
Matches 6; Conserv
JS-08-853-948B-4
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US-08-853-948B-5
RESULT 1:
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Query Match
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Sequence 10, Application US/09394272
Patent No. 6472588
GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REPERENCE: 201304/100
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
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                 66.7%; Score 36; DB 3; Length 348; 66.7%; Pred. No. 19; 1; Indels tive 2; Mismatches 1; Indels
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                                                      1; Indels
                                                                                                                                                                                                                                                       GENERAL NO. 923013)
GENERAL NO. 923013)
GENERAL TRPORMATION:
APPLICANT: Orozco Jr., Emil M.
APPLICANT: Calmi, Perry G.
APPLICANT: Weng, Zude
APPLICANT: Tarczynski, Mitchell
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
FILE REFRENCE: BB1166 US NA
CURRENT FILING DATE: 2000-10-26
FRIOR PLILNG DATE: 1998-MAY-07
FRIOR FILING DATE: 1998-MAY-06
FRIOR FILING DATE: 1999-MAY-06
FRIOR FILING DATE: 1999-MAY-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
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Query Match
Best Local Similarity 66...
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                                                                                                                             234 VIPPGMDFS 242
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US-09-394-272-10
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Zea mays
US-09-697-367-24
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US-09-394-272-10
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Sequence 11, Application US/08429054A
Patent No. 5917126
GENERAL INPORMATION:
APPLICANT: JEAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: JEAN; VOELKER, TONI; GERVAIS, MONICA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),
TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
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MEDUM TYPE FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,054A
FILING DATE: 26-APR-1995
FILING DATE: 19-March-1991
FILING DATE: 19-March-1991
FILING DATE: 19-March-1991
CLASSIFICATION NUMBER: PCT/FR 91/00593
FILING DATE: 19-UJV-1991
CLASSIFICATION NUMBER: French 90402094.9
FILING DATE: 20-JuJy-1990
CLASSIFICATION NUMBER: French 90402094.9
FILING DATE: 20-JuJy-1990
CLASSIFICATION NUMBER: 19,683
REFERENCE/ADCKET NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1137
TELECOMMUNICATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1137
TELECOMMUNICATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1137
TELECOMMUNICATION NUMBER: 12,683
REFERENCE/DOCKET NUMBER: 146.1137
TELECOMMUNICATION NUMBER: 12,683
REFERENCE/DOCKET NUMBER: 13,683
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GENERAL INFORMATION:
APPLICANT: Lando, D.
APPLICANT: Bruneau, J. M.
APPLICANT: Woelker, T.
APPLICANT: Gervais, M.
TITLE OF INVENTION: MODIFICATION O
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Matches 6; Conservative
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TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10016
COMPUTER READABLE FORM:
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435 VIPPGMDFS 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-429-054A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-718-777-7
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Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-051-341-7
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435 VIPPGMDFS 443
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435 VIPPGMDFS 443
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                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Zea mays US-09-394-272-8
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Patent No. 6124528

GENERAL INFORMATION:
APPLICANT: Shewmaker, C. K.
TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE:
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEB: Rae-Venter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
CITY: Palo Alto
CONTEXT: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYNTEM: PC-DOS/NS-DOS
COMPUTER: SYNTEM: PC-DOS/NS-DOS
COMPUTER: SYNTEM: PC-DOS/NS-DOS
COMPUTER: SYNTEM: PC-DOS/NS-DOS
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Pred. No. 68;
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                                                                                                                                       COUNTRY: California

COUNTRY: USA

ZIF: 94306

COMPUTER REDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/718,777

FILING DATE: UNT YET ASSIGNED

CLASSIFICATION: 800

PRIOR APPLICATION BOTA:

APPLICATION NUMBER: US/08/115,471

FILING DATE: 27-DEC-1993

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341
                                                                                  E: Law Offices of Barbara Rae-Venter 260 Sheridan Avenue, Suite 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.072.02US
TELECOMMUNICATION INFORMATION:
  PHOSPHATE
SYNTHASE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415)328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1068 amino acids
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                         NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               435 VIPPGMDFS 443
                                                                                         Aben...
STREET: 260 C...
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VVPXGMDYS 11
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-718-777-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-051-341-7
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Sequence 8, Application US/09394272;
Patent No. 6472588
GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED: TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE: FILE REFERENCE: 201304/1000;
CURRENT APPLICATION NUMBER: US/09/394,272;
CURRENT FILING DATE: 1999-09-10;
NUMBER OF SEQ ID NOS: 14;
SOFTWARE: Patentin Ver. 2.0;
SEQ ID NO 8;
LENGTH: 1068
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Sequence 4, Application US/09394272

Patent No. 6472588

GENERAL INPORMATION:

APPLICANT: Haigler, Candace H.

APPLICANT: Holaday, A. Scott

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

FILE REPERENCE: 201304/1000

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT PILIOR DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0
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Pred. No. 68;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 3; Length 1068;
Pred. No. 68;
2; Mismatches 1; Indels
PILING DATE: 25-OCT-1996

APPLICATION NUMBER: US 08/549,016

FILING DATE: 27-OCT-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,200

FILING DATE: 12-7AN-1995

ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,750

REGISTRATION NUMBER: 32,750

REPRENENCE/DOCKET NUMBER: CGNE.110.02US

TELEPRANCE (415)328-4400

TELEPRANCE (415)328-4477

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 amino acids
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STATE: PACOUNTRY:
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APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haigler, Candace H,
APPLICANT: Haigler, Candace H,
APPLICANT: Haigler, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION UNMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.0
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Pred. No. 69;
2; Mismatches 1; Indel8
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                                                                                                                             Score 36; DB 4; Length 1081;
Pred. No. 69;
2; Mismatches 1; Indels
; SEQ 1D NO 4
; LENGTH: 1081
; TYPE: PRT
; CRANISM: Craterostigma plantagineum
US-09-394-272-4
                                                                                                                                                                                                                                                                                                                                                 US-09-394-272-11
; Sequence 11, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-394-272-9; Sequence 9, Application US/09394272
; Sequence 9, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative 5
                                                                                                                                 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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445 VIPPGMDFS 453
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483 VIPPGMDFS 491
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US-09-394-272-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 11
LENGTH: 1083
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TILE OF INVESTION: HUMANISED ANTIBODIES
NUMBER OF SEGUENCES. 95
CORRESPONDERS NO. 618077119. LLP
TILE OF INVESTION: HUMANISED ANTIBODIES
NUMBER OF SEGUENCES. 95
CORRESPONDERS NO. 618077119. LLP
TILE OF INVESTION: HUMANISED ANTIBODIES
NUMBER OF SEGUENCES. 95
CORRESPONDERS NO. 618077119. LLP
TILE OF INVESTION: HUMANISED ANTIBODIES
NUMBER: OF SEGUENCES. 95
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MEDITAL THESE PLOPED HIM SEGUENCES. 95
COMPUTER: IRM FC Competible COMPUTER: IRM FC Competible COMPUTER: IRM FC COMPUTE
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Search completed: December 22, 2003, 16:43:43 Job time : 10.1333 secs
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US-09-252-991A-31637

Squence 31637, Application US/09252991A

Patent No. 6521795

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31637

LENGTH: 1065
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                                                                                                                                                                                                                                                                                                                                                                                               63.0%; Score 34; DB 3; Length 140; 75.0%; Pred. No. 16; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08963851
; Sequence 14, Application US/08963851
; Patent No. 6300116
; GENERAL INFORMATION:
APPLICANT: VAN DER OSTEN, CLAUS
; APPLICANT: ANDERSEN, CARSTEN
APPLICANT: ANDERSEN, CARSTEN
; APPLICANT: BAUDITZ, PETER
; APPLICANT: BAUDITZ, PETER
; APPLICANT: BAUSEN, PETER KAMP
; ITLE OP INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
; FILE REFERENCE: 4946,200-US
; CURRENT APPLICATION NUMBER: US/08/963,851
; CURRENT FILING DAME: 1997-11-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PaetSEQ for Windows Version 3.0
; SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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CLASSIPICATION: 536

ATORNEY/AGENT INFORMATION:
MAME: TRUJI110, Doreen Yarko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
FELECOMMUICATION INFORMATION:
TELECOMMUICATION INFORMATION:
TELEPHONE: (215) 568-3100
FELEPAX: (215) 568-3439
INFORMATION FOR ESQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
HOLECULE TYPE: protein
US-08-569-147-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.03
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 WPTGFDY 129
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Best Local Similarity
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                                                         Score 33; DB 4; Length 59;
Pred. No. 9.6;
4; Mismatches 2; Indels
TYPE: PRT ORGANISM: Enterococcus faecalis
                                                           Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                         |::||::||
38 EKHIPGGLEYS 48
                                                                                                                      1 BEVVPXGMDYS 11
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us-09-909-164-12.rapb

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December 22, 2003, 16:40:14; Search time 20.8667 Seconds (without alignments) 98.451 Million cell updates/sec
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| cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubpaa/USO6_NEW PUB.pep:*
3: /cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/prodata/2/pubpaa/USO7_NEW PUB.pep:*
6: /cgn2_6/prodata/2/pubpaa/USO7_NEW PUB.pep:*
7: /cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*
15: /cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*
16: /cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*
16: /cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*
17: /cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*
18: /cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*
18: /cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*
18: /cgn2_6/prodata/2/pubpaa/USO0_NEW_PUB-pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              696363 seqs, 186758610 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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54
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 946, App	Sequence 15, Appr	Sequence 10, Appl	Sequence 71, Appl	Sequence 8, Appli	Sequence 4, Appli	Sequence 11, Appl	Sequence 9, Appli	Sequence 27, Appl	Sequence 1660, Ap	Sequence 58, Appl	Sequence 5111, Ap	Sequence 4, Appli	Sequence 4, Appli
SUMMARIES	US-10-393-840-946	US-10-289-757-168	US-10-217-700-10	US-10-289-757-71	US-10-217-700-8	US-10-217-700-4	US-10-217-700-11	US-10-217-700-9	US-09-813-408-27	US-10-094-749-1660	US-10-091-007-58	US-09-815-242-5111	US-10-029-120-4	US-10-027-806-4
0.8	125	17	15	12	15	15	15	15	11	12	12	9	12	14
* Query Match Length DB ID	126	938	1049	1062	1068	1081	1083	1084	440	588	222	1062	3472	3472
% Query Match	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	64.8	63.8	63.0	63.0	63.0	63.0
Score	36	36	36	36	36	36	36	36	35	34.5	34	34	34	34
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Gaps

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Score 36; DB 12; Length 126; Pred. No. 14; 2; Mismatches 1; Indels

Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative

3 VVPXGMDYS 11 | : | | | | : | 23 VIPPGMDFS 31

8 8

RESULT 2 US-10-289-757-73

AP A	Sequence 526, App Sequence 526, App	Polygaccharides
623-4 801-4 0801-4 080-14 386-120 42-1069 42-1069 42-1069 42-526 697-526 698-526	US-09-978-1218-1818-1818-1818-1818-1818-1818-18	10393840 2A1 1d N. 1d N. 1d And Methods for the ation of Plant Cell Wall 10/2/10/393,840 3 09/636,800 10 10 10 10 10 10 10 10 10 10 10 10 1
2772 11 2772 11 2883 11 2822 11 286 11 386 11 386 11 386 11	736 736 736 736 736 736 736 736 736 736	
		-840-946 -846, Application U tion No. U2200302299 INFORMATION: ANT: Blokeberg, Leon OF INVENTION: Maderi OF INVENTION: Maderi OF INVENTION: Maderi OF INVENTION: Maderi OF INVENTION: MAGERI T APPLICATION UMBER: FILING DATE: 1090-08 APPLICATION UMBER: FILING DATE: 1999-10 APPLICATION UMBER: FILING DATE: 1999-10 OF SEQ ID NOS: 956 NO SEQ ID NOS: 956 NO 946 H: 126
6789010W486786	44444444444444444444444444444444444444	RESULT 1 US-10-393-840-946 Sequence 946, Application US/ Publication No. US20030229922; GENERAL INFORMATION: TITLE OF INVENTION: Material; TITLE OF INVENTION: Material; TITLE OF INVENTION: Material; TITLE OF INVENTION: Material; CURRENT APPLICATION UMBER: CURRENT APPLICATION UMBER: PRIOR PILING DATE: 2000-08-19; PRIOR PILING DATE: 1999-08-19; PRIOR APPLICATION NUMBER: US; PRIOR PILING DATE: 1999-08-19; PRIOR PILING DATE: 1999-10-09; NUMBER OF SEQ ID NOS: 956 SOFTWARE: PREFERENT TYPE: PRT

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Sequence 10, Application US/10217700
Fublication No. US20030070191A1
GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
TITLE OF INVENTION: FRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT PAPLICATION NUMBER: US/10/217,700
CURRENT PAPLICATION NUMBER: 09/394,272
SARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 1049
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66.7%; Pred. No. 1.58+02;
tive 2; Mismatches 1; Indels
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JEDDICACTION NO. US20030180751A1

GENERAL INFORMATION:

APPLICANT: Demmer, Jeroen

APPLICANT: Scherk, Richard L.

APPLICANT: Shenk, Michael Andrew

APPLICANT: Salsbury, Keith Martin

APPLICANT: Salsbury, Keith Martin

APPLICANT: Salsbury, Keith Martin

APPLICANT: Salsbury, Solutions isolated from forage

TITLE OF INVENTION: Opmositions isolated from forage

TITLE OF INVENTION: Grasses and methods for their use

FILE REFERENCE: 11000.1061U

CURRENT FILING DATE: 2002-11-07

FRIOR FILING DATE: 2001-11-07

FRIOR FILING DATE: 2001-11-07

FRIOR FILING DATE: 2001-11-07

FRIOR FILING DATE: 2001-11-07

SOFTWARE FEASTER FASTER FOR Windows Version 4.0
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%Sequence 8, Application US/10217700
% Publication No. US20030070191A1
% GENERAL INFORMATION:
% APPLICANT: Haigler, Candace H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPB: PRT
ORGANISM: Festuca arundinacea
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Best Local Similarity 66.7°
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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466 VIPPGMDFS 474
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ORGANISM: Oryza sativa
US-10-217-700-10
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LENGTH: 1062
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           US-10-217-700-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 66.7%; Score 36; DB 12; Length 937; Local Similarity 66.7%; Pred. No. 1.3e+02; nes 6; Conservative 2; Mismatches 1; Indels
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APPLICANT: Dement. Jeroen
APPLICANT: Gibson. John Bryan
APPLICANT: Gibson. John Bryan
APPLICANT: Gibson. John Bryan
APPLICANT: Glenk, Michael Andrew
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Grasses and methods for their use
FILE REFERENCE: 11000.1061U
CURRENT FILING DATE: 2002-11-07
PRIOR PLING DATE: 2001-11-07
PRIOR PLING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 168
LENOTH: 938
TYPE: PRT
Sequence 73, Application US/10289757
Publication No. US20030180751A1
GENERAL INFORMATION:
APPLICANT: Demmer, Jercen
APPLICANT: Gibson, John Bryan
APPLICANT: Gibson, John Bryan
APPLICANT: Glbson, Matchew
APPLICANT: Shenk, Michael Andrew
APPLICANT: No. US20030180751A1riss, Geoffrey
APPLICANT: Shenk, Michael Andrew
APPLICANT: No. US20030180751A1riss, Geoffrey
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Grasses and methods for their use
FILE REPREBRICE: 1000.1061U
CURRENT APPLICATION NUMBER: 60/337,703
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 937
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Sequence 168, Application US/10289757

Publication No. US20030180751A1

GENERAL INFORMATION:
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US-10-289-757-73
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462 VIPPGMDFS 470
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Matches

RESULT 3

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RESULT 4

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; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-217-700-11
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LENGTH: 440
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Sequence 11, Application US/10217700

Publication No. US2030070191A1

GENERAL INFORMATION:

APPLICANT: Haigler, Candace H.

APPLICANT: Holaday, A. Scott

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

FILE REFERENCE: 201304/1000

CURRENT PILING DATE: 2002-09-12

EARLIER APPLICATION NUMBER: 09/394,272

EARLIER FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10217700
Publication No. US20030070191A1
GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700
CURRENT PILING DATE: 2002-08-12
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER APPLICATION NUMBER: 09/394,272
SARIER PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOUTHARE: Patentin Ver. 2.0
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APPLICANT: Holaday, A. SCOTT

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700
EARLIER APPLICATION NUMBER: US/202-08-12
EARLIER PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
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Pred. No. 1.6e+02;
2; Mismatches 1; Indels
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Best Local Similarity 66.7%;
Matches 6; Conservative ;
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Matches 6; Conservative
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435 VIPPGMDFS 443
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; ORGANISM: Zea mays
US-10-217-700-8
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LENGTH: 1081
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APPLICANT: Delagrave, Simon
APPLICANT: Delagrave, Simon
APPLICANT: Marrs, Barry
TITLE OF INVENTION: Methods For The Synthesis Of Polynucleotides And Combinatorial
TITLE OF INVENTION: Of Polynucleotides
FILE REFERENCE: HER0041
CURRENT APPLICATION NUMBER: US/09/813,408
CURRENT PILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.0
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Sequence 9, Application US/10217700

Publication No. US20030070191A1

GENERAL INFORMATION:

APPLICANT: Haigler, Candace H.

APPLICANT: Holaday, A. Scott

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

FILE REFERENCE: 201304/1000

CURRENT FILING DATE: 2002-08-10

EARLIER APPLICATION NUMBER: 09/394,272

EARLIER FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9
                                                         Gapв
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       Length 1083;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.8%; Score 35; DB 11; Length 440; 66.7%; Pred. No. 92; tive 2; Mismatches 1; Indel8
Query Match
66.7%; Score 36; DB 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 27, Application US/09813408; Publication No. US20030049619A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT GRGANISM: Aeropyrum pernix US-09-813-408-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                           483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453 VIPPGMDFS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
US-10-217-700-9
                                                                                                 3 VVPXGMDYS 11
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APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Robert A.
APPLICANT: Schleger, Christa
TITLE Schleger, Christa
TITLE ROP INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/029,120
CURRENT PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
Gaps
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DAISELDECK, NOUSEL
APPLICANT: Oblien, Kari L.
APPLICANT: Zyekind, Judith W.
APPLICANT: Zyekind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: DECARYOTES
TITLE OF INVENTION: DAISE: 2000-03-21
PRIOR REPERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-27
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-17
PRIOR PLING DATE: 
   2; Indels
   3; Mismatches
                                                                                                                                                                                                                                US-09-815-242-5111
; Sequence 5111, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 63.0
Best Local Similarity 85.7
Matches 6; Conservative
   5; Conservative
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201 KKIVPIGFDY 210
                                                      1 REVVPXGMDY 10
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; ORGANISM: Pseu
US-09-815-242-5111
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Pred. No. 1.6e+02;
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Pred. No. 68;
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                                                                                                                                                          APPLICANT: ISOGAL, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZIKO
APPLICANT: ISHII, SHIZIKO
APPLICANT: HO, YUKO
APPLICANT: HO, YUKO
APPLICANT: HO, YUKO
APPLICANT: OTSUKA, KAORU
APPLICANT: OTSUKA, KAORU
APPLICANT: SEKI, NAOHIKO
APPLICANT: SEKI, NAOHIKO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGAHARI, KENUI
APPLICANT: MASUHO, YASHHKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REPERENCE: 084355/016
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2001-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-091-007-58

US-10-091-007-58

Sequence 58, Application US/10091007

PUBLication No. US20030170782A1

GENERAL INFORMATION:

APPLICANT: Microbial Technics limited

APPLICANT: Hanniffy, Sean B

TITLE NET PILLOR Proteins

CURRENT APPLICATION NUMBER: US/10/091,007

CURRENT APPLICATION NUMBER: US/10/091,007

CURRENT FILING DATE: 1999-09-07

NUMBER OF SEQ ID NOS: 276

SEQ ID NO 58

LENGTH: 222
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                                                                              Sequence 1660, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
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; ORGANISM: Streptococcus agalactiae
US-10-091-007-58
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50.0%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1660
LENCTH: 588
TYPE: PRT
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Best Local Similarity 80.0
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US-10-094-749-1660
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Best Local Similarity
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Sequence 4, Application US/10027806;
Publication No. US2002016047641
; GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP. 1057, 806
CURRENT APPLICATION NUMBER: US/10/027, 806
CURRENT FILING DATE: 2001-12-21
FRIOR PILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
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                                                                                                                                                            Gaps
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Pred. No. 1.5e+03;
4; Mismatches 2; Indels 0; Gaps
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                                                                                                           Query Match 63.0%; Score 34; DB 12; Length 3472; Best Local Similarity 45.5%; Pred. No. 1.5e+03; Matches 5; Conservative 4; Mismatches 2; Indels C
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-029-120-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4
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Best Local Similarity 45.5%;
Matches 5; Conservative
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2294 EDVIPRGISFS 2304
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US-10-027-806-4
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Search completed: December 22, 2003, 17:32:43 Job time : 20.9333 secs

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virus

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OM protein

Run on:

Sequence:

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Result

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/note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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ABB80522
ABB80525
ABB80524
ABB80544
ABB80554
ABB80554
ABB80555
ABB80555
ABB80555
ABB80556
ABB80556
ABB80566
ABB80559
ABB80559
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ABB80554
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  19-JUL-2001; 2001WO-US23169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
  11
/note=
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Misc-difference
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Modified-site
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  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB80524
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ABB80524
 Hepatitis C virus
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                                                                       2003, 16:41:00 ; Search time 32.4667 Seconds (without alignments) 53.778 Million cell updates/sec
                                                                                                                                                                                                                                                                                                             A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1985.DAT:*
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| SIDSI/gcgdata/geneseq-embl/AA1989.DAT:*
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| SIDSI/gcgdata/geneseq-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1991.DAT:*
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| SIDSI/gcgdata/geneseq-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1999.DAT:*
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                                                                                                                                                                                                                   1107863
          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                            1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                    using sw model
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ABB80529
ABB80561
ABB80562
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ABB80543
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Gapop 10.0 , Gapext
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Maximum DB seq length: 200000000
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54
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                                                    - protein search,
                                                                          December 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery
Match
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96.3
96.3
96.3
96.3
87.0
87.0
                                                                                                                               score:
                                                                                                                                                             Scoring table:
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52
52
52
52
54
74
47
46
46
46
47
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virus virus

virus virus virus

virus virus virue

virus virus virus virus virus virus

Hepatitis Hepatitis

Gaps

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Length 11; Indels

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
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Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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100.0%; Pred. No. 0.0018;
ive 0; Mismatches 0
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                                                                     Claim 17; Page 64; 69pp; English.
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hes 11; Conservative
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                                     (CORV-) CORVAS INT INC
                                                                        Levy OE,
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of
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                                                           a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                   Score 52; DB 23; Length 11;
Pred. No. 0.0018;
0; Mismatches 0; Indels
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100.0%; Pre
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les 11; Conserv
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    residue 7"
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is useful for treating disorders associated with hepatitis C virus.
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Pred. No.
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                                              96.3%; Sccilarity 100.0%; Pr
Conservative 0;
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                       "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22
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                                                 ABB80542 standard; peptide; 11 AA.
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Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                                                                                                                                                      virucide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
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                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
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Score 52; DB 23; Length 11;
Pred. No. 0.0018;
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Pred. No. 0.017;
0; Mismatches 1; Indels
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          100.0%; Pred. ...
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                 Local Similarity
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                carbonyl forming keto-amide linkage with 7"
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Pred. No. 0.026;
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/note= "D-form residue"
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90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                             Norvalyl carbonyl forming keto-amide linkage with residue 7"
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                                            Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23
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The sequence represents a peptide compound of the invention having the peptides of the invention are alpha-ketoamide peptide analogues. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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Pred. No. 0.026;
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90.9%;
               21-JUL-2000; 2000US-220101P.
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residue 7"
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/note= "C-terminal amide"
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90.9%;
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Matches

RESULT 11

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Gaps

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Indels

7

0; Mismatches

Score 46; DB 23; Length 11; Pred. No. 0.026;

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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                         C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28.
                                                                                                                                                                                                                              ABB80548 standard; peptide; 11 AA.
                                                                                                      85.2%;
90.9%;
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                                                                                                  Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                 The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of invention are alpha-ketcamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredis useful for treating disorders associated with hepatitis C virus.
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                                  Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
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Pred. No. 0.026;
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/note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
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         Score 46; DB 23; Length 11;
Pred. No. 0.026;
0; Mismatches 1; Indels
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Query Match
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; Search time 9.06667 Seconds (without alignments) 116.675 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                December 22, 2003, 17:24:36
                                                                        OM protein - protein search, using sw model
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54
1 EEVVPXGMDYS 11
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000 PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	conserved hypothet	V1 protein - tobac	sucrose-phosphate	sucrose-phosphate	unknown protein F2	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	hypothetical prote	peptidoglycan-bind	probable alkaline	hypothetical prote	probable membrane	fat facets (faf) s	plastocyanin b - L	plastocyanin precu	plastocyanin b pre	6-0-methylguanine-	O6-methylguanine-D	hypothetical prote	probable hexosyltr	L-lactate dehydrog	ABC transporter AT	phenylalanine-tRNA	succinate dehydrog	disease resistance
SUMMARIES	ID	S54619	D69551	A42452	\$72649	872650	G96764	JC4783	JQ1329	T09837	T04062	T04103	T24111	H87660	H72784	T20173	F69009	B49132	800210	838255	S58208	AG3104	D98182	P72745	G69290	G69350	E86665	A70164	F81138	T48898
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	당성	74.1	70.4	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	64.8	64.8	64.8	64.8	64.8	64.8	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0
	Score	40	38	36	36	36	. 36	36	36	36	36	36	35	35		35		35		34	34	34	34	34	34	34	34	34	34	34
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disease resistance RND multidum offl	hypotherical prote hymotherical 1678	partial transposas	fibroblast growth	hypothetical prote	hypothetical prote	conserved hypothet	unknown protein [i	transposase ISC105	transposase ISC105	hypothetical prote	pantoate-beta-alan	transposase ISC105
T48899 P81315	T30830	A99427	\$27021	E90335	S57810	A96001	A96546	F90298	C90307	C64417	G83055	E90487
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908	1062	97	172	184	225	247	257	262	267	276	283	299
63.0	63.0	1.13	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1
9. A.	9 P		33	33	33	33	33	33	33	33	33	33
30	333	. 6. c.	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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2 EVVPXGMDY 10

Š 셤 conserved hypothetical protein AF2411 - Archaeoglobus fulgidus

us-09-909-164-12.rpr

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Bucrose-phosphate synthase (EC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
C;Species: Citrus unshiu
C;Species: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: 572650
R;Komateu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A;Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate synt A;Reference number: 572648; MUID:96439842; PMID:8842155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hoxosyltransferase; sucrose biosynthesis
F;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                                                                                                                                                                                                                                           A.Fetatus: nucleic acid sequence not shown
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-348 «KOM»
A.Fesidues: 1-348 «KOM»
A.Fross-references: EMBL.AB006660; NID:g2351059; PIDN:BAA22071.1; PID:g2351060
A.Fxperimental source: fruit, cv. Miyagawa-Wase
A.Rote: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 66.7%; Score 36; DB 2; Length 348; Best Local Similarity 66.7%; Pred. No. 17; Matches 1; Indels Matches 1; Indels
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Best Local Similarity 70.0
Matches 7; Conservative
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234 VIPPGMDFS 242
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C;Punction:
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VI protein - tobacco yellow dwarf virus (strain Australia)

C,Species: tobacco yellow dwarf virus (strain Australia)

C,Species: tobacco yellow dwarf virus

C,Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999

C,Pacession: A4245

R,Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.B.

Virology 187, 633-642, 1992

A,Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yelld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Citrus unshiu (fragment)
C;Species: Citrus unshiu
C;Species: Citrus unshiu
C;Species: Citrus unshiu
C;Accession: S72649
R;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
A;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
A;Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
A;Title: Cloning and molecular analysis of CDNAs encoding three sucrose phosphate syntha A;Reference number: S72649; MUID:96439842; PMID:8842155
A;Accession: S72649
A;Acce
A;Molecule type: DNA
A;Residues: 1-363 «KLE»
A;Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068
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(S,Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;1-141/Domain: sucrose-ksucrose-phosphate synthase homology (fragment) <SSPS>
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A;Residues: 1-102 <MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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                                                                                                                                                      Query Match 70.4%; Score 38; DB 2; Length 363; Best Local Similarity 54.5%; Pred. No. 6.8; Matches 6; Conservative 3; Mismatches 2; Indels
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Pred. No. 4.3;
3; Mismatches 1; Indels
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60.0%;
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Matches 6; Conservative
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120 ENIVPYGIDFS 130
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228 VIPPGMDFS 236
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A,Gene: SPS2
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unknown protein F25P22.17 [imported] - Arabidopsis thaliana
Unknown protein F25P22.17 [imported] - Arabidopsis thaliana
G;Species: Arabidopsis thaliana (mouse-ear cress)
G;Accession: 40.4 Marabologis thaliana (mouse-ear cress)
G;Accession: 40.4 Marabologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons
G;Accession: 40.4 Mar.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K
ansen, N.F.; Hughes, B.; Hulzar, L.
A;Authors: Hughes, B.; Hulzar, L.
A;Authors: Hughes, T.; Jenk, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
ker, M.; Wu, D.; Yu, G.; Frager, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-460 <STO>
A;Coss-references: GB:AE005173; NID:g6692750; PIDN:AAF24856.1; GSPDB:GN00141
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70.0%; Pred. No. 23;
ive 0; Mismatches 3; Indels
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C;Species: Oryza sativa (rice)
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RESULT 5

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Bucrose-phosphate synthase homolog F28M11.40 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999 C;Accession: T04062 R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F submitted to the Protein Sequence Database, March 1999
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A;Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3;
A;Note: P28M11.40
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C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
P;176-674/Domain: sucrose/sucrose-phosphate synthase homology <SSS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-f1
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F;230-714/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
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C;bace: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Accession: T04103
R;Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T.
Plant Sci. 112, 207-217, 1995
A;Ttle: Structure 307-217, 1995
A;Reference number: 215.212
                            A.Title: Analysis of cDNA clones encoding sucrose-phosphate synthase in relation the Ariticle: Analysis of cDNA clones encoding sucrose-phosphate synthase in relation the Reference number: Z16874; MUID:97451773; PMID:9306694
A.Recession: T09837
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary
A.Status: A.Status: AND.
A.Status: A.Status: AND.
A.Status: A.Status: AND.
A.Status: A.Status: AND.
A.Status: A.S
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A,Accession: T04062
A,Molecule type: DNA
A,Residues: 1-1083 <BEV>
A,Residues: 1-1083 <BEV>
A,Residues: 0.1083 <BEV>
A,Residuestics: 0.1083 <BEV
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; Pred. No. 60;
2; Mismatches
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A;Cross-references: EMBL:D45890; PIDN:BAA08304.1
A;Experimental source: subsp. Japonica
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Best Local Similarity 66.7%;
Matches 6; Conservative 5
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Best Local Similarity 66.7
Matches 6; Conservative
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483 VIPPGMDFS 491
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                 Physiol. 115,
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                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-1049 «VML»
A; Cross-references: GB:U3175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
A; Note: UDPglucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDPglucosylt
C; Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
C;Accession: JC4783
R;Valdez-Aharcon, J.J.; Perrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella Gene 170, 217-222, 1996
A;Title: Characterization of a rice sucrose-phosphate synthase-encoding gene.
A;Reference number: JC4783; MUID:96235138; PMID:8666248
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A, Molecule type: protein
A, Residues: 71-74;206-212;471-481;872-892 < WOR1>
C, Comment: This enzyme transfers the glucosyl group from UDPglucose to fructose-6-phosph
C, Comment: This enzyme is involved in the regulation of carbon partitioning in the leave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
A;Pathway: sucrose biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Function:
A;Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introne: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3; C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F;180-663/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
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C;Species: Craterostigma plantagineum
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09837
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A, Residues: 1-1068 <WOR>
A, Cross-references: GB:M97550; NID:g168625; PIDN:AAA33513.1; PID:g168626
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R;Ingram, J.; Chandler, J.W.; Gallagher, L.; Salamini, F.; Bartels, D.
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Pred. No. 59;
2; Mismatches 1; Indels
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Matches 6; Conservative
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436 VIPPGMDFS 444
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435 VIPPGMDFS 443
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probable alkaline proteinase APE0263 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Accession: H72784
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tak.
Bwa, H; Takamiya, M.; Masuda, S.; Runahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA, Res. G, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72784
A;Accession: H7284
A;Accession: H72784
A;Accession: H72784
A;Accession: H72784
A;
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Similarity 66.7%;
6, Conservative
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Best Local Similarity
Matches 6; Conserv
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A,Gene: APB0263
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heldelberg, J.
Bs; Laub, M.T.; DeBoy, K.T.; DeBoy, K.J.; DeBoy, K.B.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                              A;Map position: 1
A;Map position: 1
A;Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
A;Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
C;Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology c;Keywords: glycosyltransferase; hexosyltransferase
F;196-680/Domain: sucrose/sucrose-phosphate synthase homology cSSPS>
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A,Molecule type: DNA
A,Residues: 1-425 <MIL>
A,Cross-references: EMBL:Z81109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
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A;Cross-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148 C;Genetics: A;Gene: CG322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein R10D12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accesion: T24111
R;Percy, C.
submitted to the EMBL Data Library, October 1996
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Pred. No. 34;
3; Mismatches
                                                                                                                                                                                                                                                                           Score 36; DB 2
Pred. No. 60;
2; Mismatches
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A;Map position: 5
A;Introns: 23/3; 56/3; 113/3; 257/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone R10D12
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54.5%;
                                                                                                                                                                                                                                                                       66.78;
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Best Local Similarity 50.0%;
Matches 5; Conservative 3
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7°
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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453 VIPPGMDFS 461
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A;Accession: T24111
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C,Genetica:
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A,Map position: 5
A,Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2;
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C,Species: Caenorhabditis elegans
C,Accession: T20173; T23857
R;Mortimore, B.
Submitted to the EMBL Data Library, November 1996
A,Reference number: 219232
A,Reference mumber: 219232
A,Reference preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-1150 (WIL)
A,Rossi-mental source: Clone C53A5
A,Residues: L.
Submitted to the EMBL Data Library, August 1996
A,Reference number: 219808
A,Reference 
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llarity 66.7%; Pred. No. 1e+02;
Conservative 2; Mismatches 1; Indels
                                                                                                                 2; Length 440
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                                                                                                           Score 35; DB 2
Pred. No. 35;
2; Mismatches
C, Superfamily: subtilisin; subtilisin homology
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                      OM protein - protein search, using sw model
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December 22, 2003, 16:43:51; Search time 4.6 Seconds (without alignments) 112.455 Million cell updates/sec US-09-909-164-12 54 1 EEVVPXGMDYS 11 Title: Perfect score: Run on:

Scoring table: Sequence:

127863 seqs, 47026705 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	ption	fusobacteri	tobacco yel	oryza sativ	zea mays (m	craterostig	_	homo sapien	•	hordeum vul	populus nig	borrelia bu	arabidopsis	arabidopsis	arabidopsis	methanococc	pseudomonas	vibrio chol	rattue norv	halomonas e	halomonas e	homo sapien	mus musculu	gallus gall	schizosacch	simian foam	vibrio chol	homo sapien	xenopus lae	daucus caro	listeria in	listeria mo	rattus norv	escherichia
	Description	Q8rg86	P31619	043802	P31927	004933	P55824	Q9nr64	P20423	P08248	P11970	P94283	Q9£jk8	Q8w4j9	P59584	058349	09hv69	Q9kmy3	P08503	052250	O9zen7	060344	061851	P18460	074377	P27399	Q9kv29	P15822	P19102	P20422	Q92bc5	Q8y6u8	004667	P08203
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<b>*</b>	Match	70.4	66.7		66.7	Ġ.	4	63.9	63.0	63.0	63.0	63.0	63.0	63.0	63.0	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1					59.3	59.3
	Score	38	36	36	36	36	35	34.5	34	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	32.5	32	32	32	32	32
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P06190 salmonella Q9wzrl thermotoga Q04827 rattus norv P30279 homo sapien P30280 mus musculu Q90459 brachydanio P50755 xenopus lae P53782 xenopus lae P53182 yenopus lae P5169 gallus gall P5189 kenopus lae P5169 gallus gall P5189 kenopus lae P5189 kenopus lae P5189 homo sapien P24385 homo sapien
ARAD SALTY H1S9 THEMA CGD2_RAT CGD2_RUMAN CGD2_MOUSE CGD1_BRARE CGD1_XENLA CGD2_XENLA CGD2_XENLA CGD2_XENLA CGD1_CHICK CGD3_XENLA CGD1_CHICK CGD3_XENLA CGD1_CHICK CGD3_HUMAN
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## ALIGNMENTS

T 1 CARE FUSNN STANDARD; PRT; 1058 AA. QBRGB6; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain). CARB OR FN0422. Rusobacterium nucleatum (subsp. nucleatum). Bacteria; Fusobacteria; Fusobacteria; Fusobacteriaceae; NCBL TaxxD=76856;	PubMed=11889109; Son I., Ivanova N., Reznik G., Los T., Lykidis A. Bartman A., Gardner W., Grechkin G., Zhu L., Kogan Y., Chaga O., Goltsman B., Bernal A., des N., Overbeek R.; des N., Overbeek R.; 2005-2018(2002). 2005-2018(2002). 2005-2018(2002). 3005-2018(2002). 3005-2018(2002). 3005-3018(2002). 3005-3018(2002). 3005-3018(2002). 3005-3018(2002). 3005-3018(30	the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).  -1- SIMILARITY: BELONGS TO THE CARB FAMILY.  This SWISS-PROT entry is copyright. It is produced through a collaboration the SWISS-PROT entry is copyright. It is produced through a collaboration the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).  EWBL; AE010554; AAL94625.1; ALT_INIT.  EWBL; AE010554; Cara L glu.  InterPro; IPR005483; CPase L D3.  InterPro; IPR005481; CPase L D3.
STANDARD;  tel. 41, Crec tel. 41, Last tel. 41, Last tel. 41, Last phate synthat thetase ammor nucleatum (t nucleatum (t bbacteria; Ft	N.A. 1986; 194; PubMed=: 194; PubMed=: 104; PubMed=: 107; Vrgides N., 108; Vrgides N., 108; 108; 108; 108; 1184:2005-201 185:2005-201 185:2005-201 185:2005-201 185:2005-201 185:2005-201 185:2005-201 185:2005-201 185:2005-201 185:2005-201 185:2005-201 1	(or ammonia) ); BELONGS TC T entry is conversed in the co
P. 1. FUGSIN STANDARD; QBRGG6; 28-FBB-2003 (Rel. 41, Ca 28-FBB-2003 (Rel. 41, Le 28-FBB-2003 (Rel. 41, Le 28-FBB-2003 (Rel. 41, Le 28-FBB-2003 (Rel. 41, Le Carbamoyl-phosphate synthetase amm Phosphate synthetase amm CARB OR FN0422. FUSObacterium nucleatum Bucceria; Fusobacteria; Fusobacterium. FUSOBACTERIUM. FUSOBACTERIUM.	[1] SEQUENCE FROM N.A. STRAIN=ATCC 25586; MEDLINE=21886394; KAPATENI V., Ander Bhattacharyya A., Vasieva O., Chu L., Larsen N., D'Souza Fonerein M., Kyrpi Genome sequence a nucleatum strain A. J. Bacteriol. 184:	the large ( similarity) -1- SIMILARITY. This SWISS-PROT The SWISS-PROT The Buropean Bi use by non-pr modified and the entities requir or send an emai EMBL, AE010554; HAWAP, W 01210 InterPro; IPRO0 INTERPRO IPRO0 INTERPRO IPRO0 INTERPRO IPRO0 INTERPRO IPRO0 INTERPRO IPRO0 INTERPRO IPRO IN
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SPS_MAIZE
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SPS_ORYSA
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R PRIMTS, PRO2142; MUS; 1.

R PRIMTS, PRO0098; CPSASE.

OR TIGREAMS, TIGRO1369; CPSASE.

OR PROSITE; PS00866; CPSASE.

OR PROSITE; PS00867; CPSASE.

OR Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;

Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Lig
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MURDLINES-29188538; PubMed=1546458;

MORTIS B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

"The nucleotide sequence of the infectious cloned DNA component of thobacco Pallow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants.";

Virology 187:633-642(1992).
                                                                                                                                                                                                                                                        ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

MANGANESE I (BY SIMILARITY).

MANGANESE I (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).

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117451 MW; ED7037AF77CLE39F CRC64;
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Pred. No. 9.1;
3; Mismatches 1; Indels
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60.0%; Pred. No. 2;
iive 3; Mismatches 1; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
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01-JUL-1993 (Rel. 26, Last sequence update)
01-CCT-1993 (Rel. 27, Last annotation update)
Hypothetical 11.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 AA.
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InterPro; IPR002621; Gemini mov.
Pfam: PF01708; Gemini mov; I.
Hypothetical protein.
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P31619;
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SEQUENCE
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DOMAIN
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REPEAT
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NP_BIND
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CHANDOLSSIMILARIES OUT OF THE LEAF.

CHANDOLSSIMILARIES OF CONCENTRATION OF METABOLITES AND LIGHT.

CHANDOLSSIMILARIES OF HOMEOFER PROSPHORYLATION IS NOT ESSENTIAL FOR ENZYME PUNCTION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucross-phosphate synthase (BC 2.4.1.14)
(UDP-glucose-fructose-phosphate glucosyltransferase).
Oryza sativa (Rice).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Score 36; DB 1; Length 1049; 66.7%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            775 779 POLY-ARG.
1049 AA; 116455 MW; ED862E2819AA4B04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orangene, v. 197002, 19700_trans_1.
Pfam; PR001394; Glyco_trans_1, 1.
Transferase; Glycosyltransferase; Phosphorylation.
DOMAIN 22 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1068 AA.
      1049 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Cv. Indica-IR36; TISSUE=Leaf;
MEDLINE=96235138; PubMed=8666248;
      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPS MAIZE STANDARD;
P31927;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U33175; AAC49379.1; -.
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      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:| |||:|
436 VIPPGMDFS 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; JC4783; JC4783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herrera-Estrella L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gramene; Q43802;
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
SPS ORYSA
043802;
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2 EVVPXGMDYS 11

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Asteridae; lamilds; Lamiales; Lamiales incertae sedis; Torenieae;
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                Craterostigma.
NCBL_TaxID=4153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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FAF DROME
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                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Sucrose synthesis.
SUBUNIT: HOMODIMER OR HOMOTETRAMER.
DEVELOPMENTAL STAGE: GERMINATING SEEDS OR MATURE LEAVES.
PTM: PHOSPHORYLATED. HOMEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR
                                                                                                                                                                                                                                                   FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREPORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF PHOTOAASIMILATES OUT OF THE LEAF.

CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP + Bucrose 6-phosphate.

ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
                                                                                                                                                                       STRAIN=CV. PIONEER 3184; TISSUE=Leaf;
MEDLINE=92338837; PubMed=1840396;
Worrell A.C., Bruneau J.-M., Summerfelt K., Boersig M., Voelker T.A.;
"Expression of a maize sucrose phosphate synthase in tomato alters
leaf carbohydrate partitioning.";
Plant Cell 3:1121-1130 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                              Zea mays (Maize).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craterostigma plantagineum.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase 2 (RC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase 2).
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase).
                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Score 36; DB 1; Length 1068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 1068 AA; 118575 MW; 074679B5E9A1D282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1081 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 24;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M97550; AAA33513.1; -. PIR; JQ1329; JQ1329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 VIPPGMDPS 443
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                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MaizeDB; 25294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPS2_CRAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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SCORENTAR
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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PASE DROWE STANDARD; PRT; 2778 AA.

PASE DROWE STANDARD;

TO 1-00V-1997 (Rel. 35, Created)

TO 28-FEB-2003 (Rel. 41, Last sequence update)

TO 28-FEB-2003 (Rel. 41, Last sequence representation update)

TO 28-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BUCTOBE 6-phosphate.

- RAYME REGULATION ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTROL OF METABOLITES AND LIGHT.

- PATHWAY: SUCTOBE SYNTHABIS.
- SUBUNIT: Homodines or homocetramer (By similarity).
- SUBUNIT: HOMOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
MEDLINE-97451773; PubMed=9306694;

MEDLINE-97451773; PubMed=9306694;

Ingram J., Chandler J. W., Gallagher L., Salamini F., Bartels D.;

Analysis of cDNA clones encoding sucrose-phosphate synthase in relation to sugar interconversions associated with dehydration in the resurrection plant Craterostigma plantagineum Hochst.";

Plant Physiol. 115:113-121(1997)

--- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE LEAF.

--- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
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InterPro; IPR001296; Glyco trans 1.
Pfam; PP00534; Glycos transfir 1; 1.
Transferase; Glycosyltransferase; Phosphorylation; Multigene family.
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MEDLINE-93202020; Pubmed=1295747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 1; Length 1081;
Pred. No. 24;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      787 790 POLY-ARG.
1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Beet Local Similarity 66.70,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 VIPPGMDFS 453
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RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ranatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Stuton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Randon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D., Randon R.C., Badare B.G., Chen L.X., Miklos G.L.G., April J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Burtis R.C., Busam D.A., Eutler H., Cadieu E., Center A., Chadra I., Rokova D., Butcher H., Cadieu E., Center A., Chadra I., Raboson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Butris R.C., Busam D.A., Buller H., Cadieu E., Center A., Chadra I., Raboson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Butris N.L., Evangelista C.C., Ferraz C., Ferriar C., Periston M. P., Backer M., Cadieu E., Cate W. D., Harris M.L., Iberguam C., Alleris N.L., Harvey D., Heiman T.J., Herrandez J.R., Harris M.L., Harvey D., Heiman T.J., Herrandez J.R., Harris M., Alleris M.L., Lasko P., Lei Y., Levitesky A.A., Li J., Miller S., Kalp D., Lai Z., Liang Y., Lin Z., Lasko P., Lei Y., Levitesky A.A., Li J., Miller S., Kalp D., Lai Z., Lasko P., Lei Y., Levitesky A.A., Li J., J., Miller S., Mohrefi A., Mount S.M., Mollow C., Millehina N.V., Moharry C., Morberson D., Merkulov G., Milshina N.V., Moharry C., Morberson D., Mohrefi B., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Wang Z.-Y., Wassarman D.A., Walnercok G.W., Walner K., Wang A., Wang Z.-Y., Wassarman D.A., Walner C., Wang S., Yao Q., Santh H., Wang Z.-Y., Wassarman D.A., Walner C., Wang S., Yao Q., Santh H., Spier E., Spradling A.C., Stapleton W., Strong R., Shu W., Schene S., Stap
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WEDLINE-20196012; PubMed=10731138;

Rubin G.M., Horg L., Brokstein P., Evans-Holm M., Frise E.,

Stapleton M., Harvey D.A.;

"A Drosophila complementary DNA resource.";

Science 287:222-2224(2000).

-I. FUNCTION: REQUIRED FOR EYE AND EMBRYO DEVELOPMENT, AND PLAYS A.

ROLE IN COMPOUND EYE ASSEMBLY AND COGENESIS RESPECTIVELY. IN THE LANGYLE FER DISKS, CELLS OUTSIDE THE ASSEMBLING FARETS REQUIRE THIS PROPERIN FOR SHORT-RANGE CELL. INTERACTIONS THAT PREVENT THE MYSTERY CELLS FROM BECOMING PHOTORECEPTORS. IT IS ALSO REQUIRED FOR NUCLEAR MIGRATION AND CELLURARIZATION IN EARLY EMBRYOGENESIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Annotation of the Drosophila melanogaster euchromatic genome: a
  The fat facets gene is required for Drosophila eye and embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Senome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1089-2778 FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Berkeley;
MEDLINE=22426069; PubMed=12537572;
                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
                      development.";
Development 116:985-1000(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           systematic review.";
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GO; GO:00.0.

( InterPro; IPR0013>...

R PEAM; PR00135...

R PR0SITE; PS00972; UCH 2 2; 1.

DR PR0SITE; PS00973; UCH 2 2; 1.

DR PR0SITE; PS00
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EWBL outstationthe Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PlyBase; FBgn0005632; faf.

60, 60:0005737; C:Cytcplasm; IDA.

GO; 60:0007349; P:Cetluarization; IMP.

GO; 00:0007349; P:Cetluarization; IMP.

GO; 00:00068583; P:mystery cell fate differentiation (sensu Dr. . .; IMP.

GO; 00:0007097; P:nuclear migration; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ -> VTRA
NNV (in 1sefcrm 3).
/FTId=vSP 005269.
IATAATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ ->
SQRQQL (in 1sofcrm 2).
/FTId=vSP 005270.
E -> 0 (IN REF 1).
T -> S (IN REF 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                        Isold=P55824-3; Sequence=VSP 005269;
-1- TISSUR SPECIFICITY: EYE DISKS AND OVARIES.
-1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-1- SIMILARITY: Belongs to peptidase family C19.
COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR
                                                    CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0
                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 1; Length 2778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 234 E -> D (IN RBF, 1).
2725 2725 T -> S (IN RBF, 1; AAPO1345)
2778 AA; 311139 MW; PFB90438BAS3A02B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                         IsoId=P55824-2; Sequence=VSP_005270;
                                                                                                                                                                                                                                     IsoId=P55824-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, 104959; AAP01345.1;
EMBL; L04958; AAP01346.1;
EMBL; L04960; AAP01347.1;
EMBL; AR003779; AAF57198.1;
EMBL; AR003779; AAF57198.1;
EMBL; AF145677; AAD38652.1;
MEROPS; C19.007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.5%;
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1394 EVIVPDGQDFS 1404
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Best Local Similarity
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                                                                                                                                                                                                                                                                Name=2;
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CONFLICT
SEQUENCE
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RESULT 7
KHL1\_HUMAN

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Gaps

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Indels

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1; Mismatches Pred. No. 34;

80.08;

Conservative

8

1 BEVVPXGMDY 10

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Best Local Similarity
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                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           MEDLINE=20277482; PubMed=10819331;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Nagase T. tikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XVII.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 605332; -...
60: GO:0003779; Fractin binding activity; NAS.
GO: GO:000379; Fractin cytoskeleton organization and biogenesis; NAS.
InterPro; IPR000510; BTB POZ.
InterPro; IPR00652; Kelch_rep.
Pfam; PP00541; FRIch_rep.
Pfam; PP01344; Kelch, 6.
SNART; SM00525; BTB; 1.
SWART; SM00512; Relch; 6.
PROSITE; PSS0097; BTB; 1.
Cytoskeleton; Actin-binding; Kelch_repeat; Repeat.
                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!-EUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF
THE BRAIN CELLS.
                                                                                          Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20347694; PubMed=10888605;
Koob M.D., Nemes J.P., Benzow K.A.;
The SCAS transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHL1).";
Hum. Mol. Genet. 9:1543-1551(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C11C43D8282F9FF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- TISSUE SPECIFICITY: Highly expressed in brain.
-i- SIMILARITY: Contains 1 BTB/POZ domain.
-i- SIMILARITY: Contains 6 Kelch repeats.
KHL1 HUMAN STANDARD; PRT; 748 AA. QSNR64; QSHX64; QSNR65; QSP238; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Kelch-like protein 1. KALH1 OR KIAAA490.
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KELCH 2.
KELCH 3.
KELCH 4.
KELCH 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF252283; AAF81719.1; -.
EMBL; AF252279; AAF81716.1; -.
EMBL; AD40923; BAA96014.1; ALT_INIT.
EMBL; AL353738; CAC1612811; -.
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 179-409 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:6352; KLHL1.
MIM; 605332; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555
601
649
701
748 AA;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=9606;
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REPEAT
REPEAT
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DB 1; Length 748;

Score 34.5;

63.9%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGUENCE OF 30-1...

STRAILS. TO 30-1...

X Mano H., Kamo M., Tsugita A., Aso K., Nozu Y.;

X The amino acid sequence of plastocyanin from rice (Oryza sativa, RT The amino acid sequence of plastocyanin from rice (Oryza sativa, RT Bubspecies japonica).";

RL Protein Seq. Data Anal. 2:385-389(1989).

CC --- FUNCTION: Participates in electron transfer between P700 and the CC CYCOChrome b6-f complex in photosystem I.

CC --- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANB SURFACE IN CHLOROPLASTS.

CC --- SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular cloning and characterization of plastocyanin precursor in
                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probom; PD001235; Copper blue; 1.
PROSITE; PS00196; COPPER BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
Transit peptide.
157 CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
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(BY SIMILARITY).
(BY SIMILARITY).
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PLASTOCYANIN-LIKE.
                                                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Plastocyanin, chloroplast precursor.
                                                                                                                                                       154 AA
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Pred. No. 8.1;
                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gramene; P20423; -.
InterPro; IPR001923; BlueCu 1.
InterPro; IPR001235; Copper_blue.
Pfam; PF00127; copper_blud; 1.
PRINTS; PR00156; COPPERBLUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-cv. Ilpoom; TISSUE-Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP093636; AAC78108.1; -.
HSSP; P00289; 2PCP.
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54.5%;
                                                                                                                                                    STANDARD;
127 REVVP-GMDF 135
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154
154
94
139
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154 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4530;
                                                                                                                                                                          P204<u>2</u>3; Q9SBB8;
01-PBB-1991 (Re]
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee J.-S.
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Pred. No.

54.5%;

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6, Conservative
Best Local Similarity
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                                                                                                                                                                                                      P11970;
                                                                                                                                                    RESULT 10
PLAT POPNI
                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
promoter region.";
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FULL. U. Blochem. 217:97-104(1993).

-i- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.

-i- SUBCELLULAR LOCATION: LOCASELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
                                                                                                                                                                                                                                                                                                          Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nielsen O.S., Gausing K.;
The precursor of barley plastocyanin: sequence of cDNA clones and
gene expression in different tissues.";
FEBS Lett. 225:159-162(1987).
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD001235; Copper blue; 1.
PROSITE; PS00196; COPPER BLUE; 1.
Chloroplast; Blectron transport; Copper; Thylakoid; Membrane;
  IndelB
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-> N (IN CV. NK 1558).
DAA7EABE5F6F4F91 CRC64;
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PLASTOCYANIN.
PLASTOCYANIN-LIKE.
COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 plastocyanin-like domain.
3,
                                                                                                                                                                                                          01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-BEB-2003 (Rel. 41, Last annotation update)
Plastocyanin, chloroplast precursor.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y00704; CAA68696.1; -.
EMBL; 228347; CAA682201.1; -.
PIR; 538255; S38255.
HSSP; P00289; 2PCF.
InterPro; IPR000923; BlueCu_1.
InterPro; IPR001235; Copper_blue.
Pfam; PP00127; copper_blue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. NK 1558;
MEDLINE=94039081; PubMed=8223592;
2;
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  Conservative
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EDAVPSGVDVS 110
                                                                                                                                                                          STANDARD;
                                      1 EEVVPXGMDYS 11
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148
120
155 AA;
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TRANSIT 1
CHAIN 59
. 9
                                                                                                                                                                        PLAS HORVU
P08248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
METAL
VARIANT
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Length 155;

Score 34; DB 1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Salicaceae; Populus.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Italica;
Dimitrov M.1. Egorov C.A., Donchev A.A., Atanasov B.P.;
Dimitrov M.1., Egorov C.A., Donchev A.A., Atanasov B.P.;
PEBS Lett. 226.17-22(1987).
-1- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.
-1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHIOROPLASTS.
-1- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYANINS AND B.
-1- SIMILARITY: Contains 1 plastocyanin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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R InterPro; IPR000923; BlueCu 1.
R InterPro; IPR001235; Copper_blue.
R InterPro; IPR001235; Copper_blue.
R PRINTS; PR00125; Copper_blue.
DR PR051TB; PS001256; COPPER BLUE; 1.
DR PR05TTB; PS00196; COPPER BLUE; 1.
DR PR05TTB; PS00196; COPPER BLUE; 1.
DR PR05TTB; PECTron transport; Copper; Thylakoid; Membrane; KW Transit peptide; Multigene family.
PT TRANSIT 16; CHAIN 70 168 PLASTOCYANIN B.
TCHAIN 70 168 PLASTOCYANIN B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=cv. Italica; TISSUB=Leaf;
Reichert J. Janzelewski V., Haehnel W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F20DA6EA2038AEEA CRC64;
3
                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                      168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        Plastocyanin B, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Populus nigra (Lombardy poplar).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z50186; CAA90565.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                     101 EDAVPSGVDVS 111
                                                            1 BEVVPXGMDYS 11
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PIR; S58208; S58208.
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153
156
161
161
168 AA;
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 70-168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAINEATCO 35210 / B31;
STRAINEATCO 35210 / B31;
STRAINEATCO 35210 / B31;
MEDLINE-98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Rielschmann R.D., Richardson D.,
Peterson J., Kerlawage A.R., Quackenbush J., Salberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Viterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.,
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                               30-MXY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--
tRNA ligase beta chain) (PheRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PP03484; B5; 1.
TIGRPAMs; TIGR00471; pheT_arch; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barbour A.G., Hinnebusch J.;
Phenylalanyl-KRNA synthetase genes (alpha and beta subunits) and
thioredoxin reductase gene Boxrelia burgdorferi.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similatity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA
CHAIN PAMILY. SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            burgdorferi.";
Nature 390:580-586(1997).
-!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP
diphosphate + L-phenylalanyl-tRNA(Phe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Tetramer of two alpha and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%; Score 34; DB 1; Length 566; 85.7%; Pred. No. 32;
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SEQUENCE 566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
                                                                                                                                                                                                                                                       566 AA.
                                                                                                                                                                                                                                                   PRT;
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InterPro; IPR005147; B5.
InterPro; IPR004531; PheT_arch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U82978; AAB41019.1; -.
EMBL; AE001153; AAC66870.1; -
PIR; A70164; A70164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
                                                                  112 EDAVPSGVDVS 122
                                                                                                                                                                                                                                                   STANDARD;
1 EBVVPXGMDYS 11
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Best Local Similarity
Matches 6; Conserv
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Gaps

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1; Indels

0; Mismatches

Conservative

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STRAIN=CV. Columbia;

Seki M., Inda K., Satou M., Sakurai T., Akiyama K., Ishida J.,

Seki M., Inda K., Satou M., Sakurai T., Akiyama K., Ishida J.,

A Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,

Hayashizaki Y., Shinozaki K.;

T. Arabidopsis thaliana full-length cDNA.";

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

C. --- FUNCTION: Pocential disease resistance protein.

C. --- FUNCTION: Pocential disease resistance NB-LRR family.

Dathopson recognition (By similarity).

C. --- SIMILARITY: Contains 3 leucine-rich (LRR) repeats.

C. --- SIMILARITY: Contains 1 NB-ARC domain.

C. --- BATABASE: NAME-LRRS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE=Functional and comparative genomics of disease resistance gene
                                                                                                                                        15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable disease resistance RPP8-like protein 4.

RPPBIA OR AT5GA862 OR K15118.9.

Arabidopsis thaliana (Mouse-ear cress).

Rukaryota, Viridiphatae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. Columbia;
MEDLINE-99087489; PubMed-9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                          "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones."; DNA Res. 5:297-308(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interro; *FANOLIFY 2.
Pfam; PR00360; LARC; 1.
Pfam; PR0031; NB-ARC; 1.
PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
45 LBUCINE-ZIPPER.
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LRR 2.
LRR 3.
ATP (POTENTIAL).
                                                                                          908 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000767; Disease resist.
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                                                                                                                           15-SEP-2003 (Rel. 42, Created)
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InterPro; IPR002182; NB-ARC.
                                                                                        STANDARD;
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45
59
623
6623
867
169 VPPCMDY 175
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
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                                                                                        RBL4 ARATH
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DOMAIN
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STRAINE-S9030193; PubMed=9811794;

MCDOWell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,

Holub B.B., Dangl J.L.;

"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooley M.B., Pathirana S., Wu H.-J., Kachroo P., Klessig D.F.; "Members of the Arabidopsis HRT/RPP8 family of resistance genes confer resistance to both viral and comycete pathogens.";
                                                                                                                                               OBW4J9; QBGWG5; Q9M5A1; Q9ZSY3; Q9ZSY4; 15-SEP-2003 (Rel. 42, Created) 15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Disease resistance protein RPP8 (Resistance to Peronospora parasitica protein 8).
                                                                                                                                                                                                              RPPB OR HRT OR AT5G43470 OR WWE20.19.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                              Gaps
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 AND RPP8-3, AND VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Bnju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki R., Allanina K., Bayashizaki thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequen features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length CDNA clones (RAFLs) sequenced by SSP consortium (Salk/Stanford/PGEC)."; submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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                      63.0%; Score 34; DB 1; Length 908; 60.0%; Pred. No. 53; ive 2; Mismatches 2; Indels
 908 AA; 104448 MW; 3111991B17239693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Di-17;
MEDLINE=20271766; PubMed=10810142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH TIP.
MEDLINE=20496823; PubMed=11041886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Cell 10:1861-1874 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Cell 12:663-676(2000).
                                             6; Conservative
                                                                                            883 EKLVPGGEDY 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clones.";
DNA Res. 7:31-63(2000)
                                                                     1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Columbia;
                        Query Match
Best Local Similarity
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 SEQUENCE
                                                                                                                                           RPP8 ARATH
                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: Disease resistance protein. Resistance proteins guard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. The interaction with TIP (TCV-interacting protein) may be essential for the recognition of the avirulence proteins, and the triggering of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=08W4J9-2; Sequence=VSP_007171, VSP_007172;
Note=Has been shown to exist only in cv. Columbia so far;
-!- DOMAIN: The LRR repeats probably act as specificity determinant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathogen recognition.

POLYMORPHISM: The strong polymorphisms present in cv. Di-17 and cv. Columbia are probably due to an unequal crossing-over between the highly related RPPs and RPHBA genes present in cv. Landsberg erecta. Such variations probably modify the specificity of
Ren T., Qu F., Morris T.J.;
"HRT gene function requires interaction between a NAC protein and viral capsid protein to confer resistance to turnip crinkle virus."; Plant Cell 12:1917-1926 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRR 1.
LRR 2.
LRP (POTRNTIAL).
WRWLLTSRNEGVGIH -> ELLWYIHEALFLLNS (in
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Missing (In isoform 2).
/FTId=VSP_007172.
                                                                                                                                                                                                                                                                                                                                                                                                     Bvent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: Interacts with the NAC protein TIP.-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q8W4J9-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homologs;
WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF089711; AAC78631.1; -. EMBL; AF244174; AAF36987.1; -. EMBL; AB0256318; BAA97426.1; -. EMBL; AY062514; AAA12552.1; -. EMBL; AX118862; BAC43449.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF089710; AAC83165.1; -.
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Pfam; PF00931; NB-ARC;
                                                                                                                                                                                                                                                                                                                         defense response.
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|::|| | || 883 EKLVPGGEDY 892

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IDGQL -> VDEQI (in cv. Landsberg erecta).

GG -> B (in cv. Di-17).

GGK -> RGB (in cv. Di-17).

GAGV -> EKGI (in cv. Landsberg erecta).

GKGV -> EKGI (in cv. Landsberg erecta).

C -> R (in cv. Landsberg erecta).

F -> L (in cv. Landsberg erecta).

F -> L (in cv. Landsberg erecta).

G -> QQ (in cv. Di-17).

G -> QQ (in cv. Di-17).

G -> C (in cv. Di-17).

G -> C (in cv. Di-17).

H -> P (in cv. Di-17).

G -> C (in cv. Di-17).

H -> P (in cv. Di-17).

N -> S (in cv. Di-17).

N -> S (in cv. Di-17).

N -> T (in cv. Di-17).

N -> L (in cv. Di-17).
    cv. Landsberg erecta).
                                                                                                                                                                                                             Freeta).
From S (in cv. Di-17 and cv. Landeberg erecta).
W -> C (in cv. Di-17 and cv. Landeberg erecta).
C -> R (in cv. Di-17 and cv. Landeberg erecta).
N -> F (in cv. Di-17 and cv. Landeberg erecta).
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EISTYS -> KITTQB (in cv. Di-17).

A -> V (in cv. Landaberg erecta).

B -> Q (in cv. Landaberg erecta).

DNYLSWQ -> NKYLRVH (in cv. Di-17).

DN -> NR (in cv. Landaberg erecta).

WQ -> SH (in cv. Landaberg erecta).

Y -> N (in cv. Landaberg erecta).

I -> K (in cv. Landaberg erecta).
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YEAK -> FLAG (in cv. Landsberg erecta).

NLRVDT -> DLSVHE (in cv. Di-17).

RVDTB -> SVNNK (in cv. Landsberg erecta)

Q -> E (in cv. Di-17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          T -> I (in cv. Di-17).
S -> R (in cv. Di-17).
S -> R (in cv. Di-17).
H -> Q (in cv. Di-17).
I -> L (in cv. Landsberg erecta).
KNKT -> RNAR (in cv. Di-17).
K -> N (in cv. Landsberg erecta).
PRFEEDYW -> WDEDFG (in cv. Landsberg
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Y -> F (in cv. Di-17).
Y -> Y (in cv. Landsberg erecta).
C -> S (in cv. Landsberg cv. Landsberg
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C -> S (in cv. Di-17 and cv. Landsberg
erecta).
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Missing (in cv. bi-17).
Missing (in cv. bi-17).
M -> K (in cv. Landsberg erecta).
XIX -> FLF (in cv. Landsberg erecta).
XG -> FR (in cv. bi-17).
                                                                                                                                                                                                                                                                                                      erecta).
DSEISTYSLFY -> YSKISAYDLFN (in cv.
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-> Q (in cv. Di-17).
-> G (in cv. Di-17).
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Pred. No. 53;
2; Mismatches
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60.0%;
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160
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Best Local Similarity
Matches 6; Congery
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Than Cell 10:1861-1874(1998).

"In Arabidopsis."

"I PuncTION: Disease resistance protein. Resistance proteins guard

"I the plant against pathogens that contain an appropriate avirulence

protein via an indirect interaction with this avirulence protein.

"That triggers a defense system including the hypersensitive

"That triggers a defense system including the hypersensitive

"That triggers a defense system including the hypersensitive

"Reponse, which restricts the pathogen growth. In contrast to

"Reponse, which restricts the pathogen growth. In contrast to

"Republikation from Peronospora parasitica."

"MISCELLANEOUS: In cv. Columbia and cv. Di-17, this protein is not

present due to an unequal crossing over between the RPPB and RPBHA

"THE PREPARTY Selongs to the disease resistance NB-LRR family."

"SIMILARITY: Contains 1 loucine-rich (LRR) repeats.

"I SIMILARITY: Contains 1 NB-ARC domain.

"THE PARASE: NAME=NIB-LRRS;

"NOTE-FUNCTIONAL and comparative genomics of disease resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND FUNCTION.
STRAIN=cv. Landsberg erects;
MEDLINE=99030193; PubMed=9811794;
MCDowell J.M., Dhandsqudham M., Long T.A., Aarts M.G.M., Goff S.,
Holub B.B., Dangl J.L.;
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of
                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots, Rosidae,
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WWW=http://niblrrs.ucdavis.edu".
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
DOMAIN 10 45 LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 ATP (POTENTIAL).
105263 MW; SB1E9P65A19A12EB CRC64;
                                   15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Disease resistance protein RPH8A (RPP8 homolog A)
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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 PRT;
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16-OCT-2001 (Rel. 40, Last ann
Hypothetical protein MJ0939.
MJ0939.
 STANDARD;
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910 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            Arabidopsis.";
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RP8H ARATH
P59584,
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Conservative

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Gaps

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                                                                                   STRAINS—JAL-1 / DSW 2661 / ATCC 43067;
STRAINS—JAL-1 / DSW 2661 / ATCC 43067;
STRAINS—JAL-1 / DSW 2661 / ATCC 43067;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Scrivage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
Overbeek R., Kirkmes B.E., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 24;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; MJ0939; -.
Pfam; PF03692; UPF0153; 1.
Hypothetical protein; Complete proteome.
SRQUENCE 276 AA; 33454 MW; 97BD69D392BC8FDF CRC64;
Archaea, Buryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.1%; 645.5%; 1
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                                                                                                                                                                                                                                                                                                                                                                 jannaschii.";
Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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141 EEIIENGMEHS 151
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                                                   NCBI_TaxID=2190;
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Search completed: December 22, 2003, 17:42:26 Job time : 4.6 secs

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December 22, 2003, 17:27:26; Search time 25.2 Seconds (without alignments) 112.642 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                   830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
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Maximum DB seq length: 200000000
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54
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Perfect score:
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SPTREMBL 23:\*

1: sp\_archeria:\*
2: sp\_barcheria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_human:\*
6: sp\_mammal:\*
7: sp\_mhc:\*
8: sp\_organile:\*
9: sp\_plant:\*
10: sp\_plant:\*
11: sp\_virus:\*
12: sp\_virus:\*
13: sp\_virus:\*
14: sp\_unclassified:\*
15: sp\_archeriap:\*
16: sp\_bacteriap:\*
17: sp\_archeap:\*
17: sp\_archeap:\*
18: sp\_archeap:\*
19: sp\_archeap:\*
10: sp\_bacteriap:\*
17: sp\_archeap:\*
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q12479 saccharomyc	Q8esv7 oceanobacil	O30260 archaeoglob	Q8dih0 synechococc	O22081 citrus unsh	O22096 citrus unsh	Q8w568 arabidopsis	Q9c9t7 arabidopsis	P93782 saccharum o	Q9sn30 arabidopsis	Q43010 oryza sativ	Q88064 oryza sativ	Q9gq04 eriocheir B	Osxpa8 clostridium	O52367 rhizobium t	Q8k143 rhizobium e
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	ID	012479	Q8ESV7	030260	QBDIHO	02208	02209	Q8W568	16060	P93782	69SN3	04301	088064	096004	QBXPAB	052367	<b>08KL43</b>
	DB	9	16	17	16	10	10	10	10	10	10	10	10	Ŋ	16	~	N
	Query Match Length DB	156	319	363	1044	341	348	452	460	1047	1083	1084	1100	219	253	298	368
*	Query	74.1	70.4	70.4	70.4	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	64.8	64.8	64.8	64.8
	Score	40	38	38	38	36	36	36	36	36	36	36	36	35	35	35	35
	Result No.	-	~	m	4	2	9	7	80	σ	10	11	12	13	14	15	16

Q9xvk4 caenorhabdi	Q9a382 caulobacter	Q9yfi3 aeropyrum p	O52680 escherichia	Q8xz15 ralstonia s	Q946j7 andrographi	Q95p46 carcinus ma	Q9u6a3 callinectes	017704 caenorhabdi	O52673 escherichia	O52666 escherichia	O27146 methanobact	Q98k29 rhizobium l	Q8tbj7 homo sapien	Q9vsy8 drosophila	Q8r915 thermoanaer	Q8e519 streptococc	Q8dzw9 streptococc	Q8gp33 lactobacill	Q8u7j0 agrobacteri		O29920 archaeoglob	029451 archaeoglob	Q98fx1 rhizobium 1	Q8tff4 trichoderma	Q8r8z2 thermoanaer		Q9jzp8 neisseria m	
09XVK4	.6 Q9A382	.7 Q9YFI3	052680	6 Q8XZL5	.0 0946J7	095246	G9U6A3	017704	052673	052666	7 027146	.6 Q98K29	Q8TBJ7	O9VSY8	.6 QBR9L5	16 Q8E5L9	.6 Q8DZW9	Q8GP33	16 Q8U7J0	17 Q9YET8	7 029920	7 029451	.6 Q98FX1	Q8TFF4	6 QBRBZ2	_	6 Q9JZP8	6 08G3J2
425 5	433 1	440 1	511 2	517 1	595 1	745 5	1031 5	1150 5	1410 2	1420 2	1474 1	1828 1	748 4	143 5	215 1	222 1	222 1	284 2	290 1		357 1	366 1	387 1	543 3	558 1	565 1	587 1	671 1
64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	63.9	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0
35	35	35	35	35	35	35	35	35	35	35	35	35	34.5	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34
11	18	19	50	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

Database :

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WEDLINE=94019318; PubMed=8413243;
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "CYC2 encodes a factor involved in mitochondrial import of yeast cytochrome c.";
Mol. Cell. Biol. 13:6442-6451(1993).
                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaces;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECTENCE FROM N.A.
De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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De haan M., Maarse A.C., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ORF YORDIBW.
                                             PRT; 156 AA.
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STRAIN=FY1679;
MEDLINE=94169519; PubMed=7764548;
                                         PRELIMINARY;
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Q12479;
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Kirkness B.P., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.T., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocsayne J.D., Weidmen J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Rujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Citrus unshiu (Satsuma orange).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                          "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.

Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.

Matanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,

Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the thermophilic cyanobacterium

Thermosynechococcus elongatus BP-1.";

DNA Res. 9:123-130(2002).

EMBL, APOOS374 BAC09170.1; -.

Complete proteome.

Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                              Interpro; IPR002103; Bac_luciferase.
Pfam, PF00296; bac_luciferase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Multidrug efflux transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                          EMBL; AR001109; AAB91255.1; -.
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Best Local Similarity 63.6%;
                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Matches 6; Conserv
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STRAIN=HTEB31 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
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MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Doosson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlawage A.R., Graham D.B., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
  Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;

"Molecular cloning of a gene, DHS1, which complements a drug-hypersensitive mutation of the yeast Saccharomyces cerevisiae.";

Biosci. Biocechnol. Blochem. 58:391-395 (1994).

EMBL; Z74920; CAA99201.1; -.

EMBL; Z74920; CAA60762.1; -.

SGD; S0005539; YOR013W.

SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
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                                                                                                                                                                                       74.1%; Score 40; DB 3; Length 156; 77.8%; Pred. No. 2.3; ive 1; Mismatches 1; Indels
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EMBL, AP004594; BAC12465.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 319 AA; 35617 MW; 3BDAE4BF13E79E37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Buryarchāeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein AF2411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Oceanobacillus.
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                                                                                                                                                                  Query Match
Best Local Similarity 77...
7; Conservative
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189 EQLVPHGIDY 198
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Schuame RAWIN N. S. Shinn P., Banh J., Bowser L., A Kim C.J., Chen H., Cheuk R., Shinn P., Banh J., Bowser L., A Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., A Bahda J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nayyen M., Onodera C.S., A Tang C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., A Tang C.J., Torlumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Arabidopsis ORP clones";

"Arabidopsis ORP clones";

"Arabidopsis ORP clones";

"Arabidopsis ORP clones";

"Bubmitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

"RMBL, AR119044; AAM131938.1;

"BRBL, AR119044; AAM131938.1;

"RMBL, RY119044; AAM131938.1;

"RRBL, RY119044; AAM131938.1;

"RR
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.X., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                             Arabidopais thallana (Mouse-ear cress).
Bukaryota, Vridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Vitidiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Suromids II; Brassicales; Brassicaceae; Arabidopsis.
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Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
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"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                      01-NAR-2002 (TrEMBLrel. 20, Created)
01-NAR-2002 (TrEMBLrel. 20, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
At1g73750/P25F22_17.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 50.6 kDa protein.
                                                                                                                                                                                                 452 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%;
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                              PRELIMINARY;
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         |:| |||:|
234 VIPPGMDFS 242
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SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
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NCBI_TaxID=3702;
                                                                                                                                                                                           08W568
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                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. Miyagawa-Wase; TISSURE-Juice sacs and segment epidermis; Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.; Tomatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.; "Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.)."; Plant Sci. 140:169-178(1999).
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Sapindales; Rutaceae; Citrus.
NCBL_TaxID=55188;
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TISSUE-Juice sacs and segment epidermis;
Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;
"Differential expression of three sucrose-phosphate synthase isoforms during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";
Plant Sci. 140:169-178(1999).

EMBL; AB006660; BAA22071.1; -.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Sapindales, Rutaceae, Citrus.
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                                                                                                                                                               epidermis
                                                                                                                                                                              MEDILINE=96439842; Pubmed: A12015. MEDILINE=96439842; Pubmed: MEDILINE=96439842; Pubmed: Medilipse Andrews A., Takanokura Y., Omura M., Akihama T.; Cloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
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TISSUB=Juice sacs and segment epidermis;

MEDLINE=96439842; PubMed=8842155;

KOMATESU A., Takanokura M., Akihama T.;

"Cloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                           STRAIN=cv. Miyagawa-Wase; TISSUE=Juice sacs and segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 AA; 38136 MW; 61417A69C4560777 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 AA
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Sucrose-phosphate synthase (Fragment).
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                                                                                                                                                                                                                                                                                                                 Marc.).";
Mol. Gen. Genet. 252:346-351(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Citrus unshiu (Satsuma orange)
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022096

RESULT 6 022096 Matches

Matches

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Gaps

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"Structure and RPLP mapping of a rice sucrose phosphate synthase (SPS) gene that is specifically expressed in the source organ."; Plant Sci. 112:207-217(1995).
EMBL; D45890; BAA08304.1; -.
                                                                                                                                                                                                                                                                                                         P28MII.40 OR AT4G10120.

Arabidopsis thaliams (Mouse-ear cress).

Bukaryots; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECURNCE FROM N.A.
BEVAN M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sakamoto M., Satozawa T., Kishimoto N., Higo K., Shimada H.,
Pujimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Score 36; DB 10; Length 10
66.7%; Pred. No. 1.5e+02;
ive 2; Mismatches 1; Indels
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InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001557; L_LDH.
Pfam; PF00534; Glyco_Ernsf_1; 1.
PROSITE; PS00064; L_LDH; 1.
SEQUENCE 1084 AA; 119417 MW; 4D0D79AFEDD2F92B CRC64;
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Submitted (MAR. 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL049487; CAB397641; -.
EMBL; AL049487; CAB397641; -.
InterPro; IPR001296; Glyco_trans 1.
Pfam; PF00534; Glycoetrans 1.
Glycosyltransferase; Transferase.
SEQUENCE 1083 AA; 122688 MW; EFC126FCA2137BB1 CRC64;
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Submitted (SRP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sucrose-phosphate synthase-like protein (EC 2.4.1.14).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sucrose phosphate synthase.
                                                                                                                     PRT; 1083 AA
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                                                                                                             PRELIMINARY;
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483 VIPPGMDFS 491
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                       Theologis A., Ecker J. A., Pandro C.J., Federspiel N.A., Kaul S., A. Theologis A., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., A. Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M. K., Conway A.B., Conway A.B., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldhlyum T.V., Feng J.-D., Fong B., Fujii C.Y., A. Gill J.E., Goldemith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., A. Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., A. Kim C.J., Loe A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin S.L., Liu S.X., Liu S.A., Maiti R., Marziali A., Milischer J., Miranda M., Nuyen M., Nerman W.C., Osborne B.I., A. Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Souley D., Sann H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Walker M., Nuyeberg M., Wysotskaia V.S., Walker M., Wu D., Yu G., Fraser C. M., Varsher J.C., Davis R.W.; Razio M., John A. K., Marziali A., Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Soulhwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Walker M., Wu D., Yu G., Fraser C. M., Venter J.C., Davis R.W.; F., Salzerg S.L., Varsher J.C., Davis R.W.; F., Shinn P., Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Walker M., Nu D., Yu G., Fraser C. M., Venter J.C., Davis R.W.; F., Salzerg S.L., Varsher J.C., Davis R.W.; F., Salzerg S.
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Sugiharto B., Sakakibara H., Sugiyama T.;
"Differential Expression of Two Genes for Sucrose-Phosphate Synthase
in Sugarcane: Molecular Cloning of the cDNAs and Comparative Analysis
of Gene Expression.
Submitted (PEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB001337; BAA19241.1;
"InterPro; IPR001296; Glyco_trans 1.
Pfam; PF00534; Glycos trans 1.
Glycosyltransferase; Transferase.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 10; Length 460;
Pred. No. 56;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1047 AA; 116379 MW; DOEDB34961E1D83D CRC64;
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EMBL, AC012679; AAG52073.1; -.

InterPro; IPR002471; Prol endopep ser.

InterPro; IPR000379; Ser estrs site.

PRCSITE; PS00708; PRO_ENDOPEP_SER; 1.

Hypothetical protein.
MEDLINE=21016719; PubMed=11130712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 70.0
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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414 VIPPGMDFS 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4547;
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SOSPS1.

P93782

RESULT 9 P93782

SEQUENCE

Query Match

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SEQUENCE

Query Match

Matches

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Gaps

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Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                   4 VPXGMDYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flesh-eater."
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052367
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Gill;
Weihrauch D., Towle D.W.;
Weihrauch D., Towle D.W.;
Wa+/H+-exchanger and Na+/K+/2Cl- -cotransporter are expressed in gills of the euryhaline Chinese crab Briocheir sinensis.";
Comp. Biochem. Physiol. 126:S158-S158(2000).
EMBL; AF301160; AG39938.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAINECV. NIPPONDAIRE;
STRAINECV. NIPPONDAIRE;
SABAKI T., MAISUNDOCO T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%; Score 36; DB 10; Length 1100; 66.7%; Pred. No. 1.5e+02; ive 2; Mismatches 1; Indels C
                     Length 1084;
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Eriocheir Sinensis (Chinese mitten crab).

Eurayota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Bucarida; Decapoda; Pleccyemata; Brachyura;

Eubrachyura; Grapsoidea; Varunidae; Eriocheir.

NCBI_TaxID=95602;
                   66.7%; Score 36; DB 10; Length 10
66.7%; Pred. No. 1.5e+02;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001557; L_LDH.
InterPro; IPR001557; L_LDH.
Pfam; PP00534; Glycos transf_1; 1.
PR051TE; P00064; L_LDH; 1.
SEQUENCE 1100 AA; 121170 MW; 084F4604BA389CAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003437; BAB86107.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 219
219 AA; 24159 MW; 599442DA26F0D3F1 CRC64;
                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Putative sucrose-phosphate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) Na+/K+/2Cl-cotransporter (Fragment).
                                                                                                                                                                                                                                                        PRT; 1100 AA.
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                                                             6; Conservative
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453 VIPPGMDFS 461
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                                                                                                     3 VVPXGMDYS 11
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Best Local Similarity
6, Conserve
                                         Local Similarity
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Matches
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Q8S064
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Gaps
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
--- COFACTOR: ZINC (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=13 / Type A;
PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohehima K., Yamashita A.,
Shibizu T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
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Similarity 50.0%; Pred. No. 46;
5; Conservative 3; Mismatches 2; Indels
  5; Length 219;
                                                        1; Indels
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EMBL; AP003185; BAB79763.1; -
InterPro; IPR0002059; NAD binding.
InterPro; IPR000594; ThiF_domain.

Fram; PR00899; ThiF; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 253 AA; 27714 MW; 814DF79D3E0D7486 CRC64;
                                                                                                                                                                                                                                                                                                                              01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNW-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein CPE0057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aryl-alcohol dehydrogenase homolog (Fragment).
  Score 35; DB 5
Pred. No. 39;
1; Mismatches
                                                                                                                                                                                                                                                                                                       253 AA.
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ов
39;
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InterPro; IPR002328; ADH zinc.
InterPro; IPR002005; Adh zin Edmily.
InterPro; IPR000205; NAD-binding.
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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108 BEIIPDDVDY 117
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DR Pfam; PF00107; adh_zinc; 1.

DR PROSITE; P800059; ADH_ZINC; 1.

KW Metal-binding; Oxidoreductase; Zinc; Plasmid.

FT NON_TER 298 AA; 31092 MW; 49B2F8117C33AB87 CRC64;

Query Match 64.8%; Score 35; DB 2; Length 298;

Best Local Similarity 50.0%; Pred. No. 55;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EVVPXGMDYS 11

Cy 2 EVVPXGMDYS 11

Db 250 EIIPEGADFS 259

Search Completed: December 22, 2003, 17:51:29

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Hepatitis

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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Total number

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88

Minimum Maximum Database

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
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ABB80522
ABB80525
ABB80547
ABB80541
ABB80548
ABB80551
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/note= '
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Misc-difference
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Modified-site
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 Synthetic
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ABB80524
 Hepatitis C virus
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                                                                                                            December 22, 2003, 16:41:00; Search time 32.4667 Seconds (without alignments) 53.778 Million cell updates/sec
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1: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

3: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDSI/gcgdata/geneseqp-embl/AA1982.DAT:*

4: /SIDSI/gcgdata/geneseqp-embl/AA1982.DAT:*

5: /SIDSI/gcgdata/geneseqp-embl/AA1982.DAT:*

6: /SIDSI/gcgdata/geneseqp-embl/AA1985.DAT:*

7: /SIDSI/gcgdata/geneseqp-embl/AA1985.DAT:*

8: /SIDSI/gcgdata/geneseqp-embl/AA1987.DAT:*

9: /SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*

10: /SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*

11: /SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*

12: /SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*

13: /SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*

14: /SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*

15: /SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*

16: /SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*

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                                                                                                                                                                                                                                                                                                                                      1107863
             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                   1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                - protein search, using sw model
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ABB80562
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length: 2000000000
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19-JUL-2001; 2001WO-US23169

Score

Result No.

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virus protease
                   virus protease
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activity
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                                                                                                                           The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha-ketoanide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                      Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
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                                                                                                                                                                                                                    Query Match 96.3%; Score 52; DB 23; Length 11; Best Local Similarity 100.0%; Pred. No. 0.0018; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "N-terminal acetyl"
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                                     Brunck TK;
                                                                                                                                                                                                                                                                                                                        ABB80528 standard; peptide; 11 AA.
                                                                                                           Claim 17; Page 64; 69pp; English
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21-JUL-2000; 2000US-220101P
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                   (CORV-) CORVAS INT INC
                                     Levy OE,
                                                                                                                                                                                                                                                                        1 EBWPXGMDYS
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                                                      WPI; 2002-361643/39
                                                                                           virus protease -
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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residue 7"
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peptide compound having hepatitis C virus protesse inhibitory
lty useful for treating disorders associated with hepatitis C
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100.0%; Pred. No. 0.0018;
ive 0; Mismatches 0; Indels
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                                                                                                                             Claim 17; Page 64; 69pp; English
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoande peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat alsorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41
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                                                                                                                                             Length 11;
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                                                                                                                                          96.3%; Score 52; DB 23;
100.0%; Pred. No. 0.0018;
iive 0; Mismatches 0;
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                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                      virucide.
                                                                                                                                            Query Match
                                                                                                                                                            Local
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'note= "Norvaly1 carbony1 forming keto-amide linkage with
    residue 7"
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                                                                            Gaps
                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
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                                      DB 23; Les.
0.0018;
                                        96.3%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Oxymethionine"
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                                                                                                                                                                                                                                            (first entry)
                                              Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                                                    1 EEVVPXGMDYS 11
                                                                                                                           1 REVVPXGMDYS 11
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                         11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200208251-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus protease
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Matches

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The sequence represents a peptide compound of the invention having the peptides of the invepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                         "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                                                    Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                  Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22.
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Pred. No. 0.017;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                         'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB80543 standard; peptide; 11 AA.
                                                 ABB80542 standard; peptide; 11 AA.
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90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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Modified-site
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residue 7"
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                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                         Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
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 DB 23; Length 11; 0.0018;
                                 0, Indels
96.3%; Score 52; DB
100.0%; Pred. No. 0.0
ive 0; Mismatches
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                                 11; Conservative
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                                                                                            EEVVPXGMDYS
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Gaps

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Length 11; 1; Indels

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"Norvalyl carbonyl forming keto-amide linkage with residue 7"
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lty useful for treating disorders associated with hepatitis C
protease
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                                                             'note= "N-terminal acetyl"
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                                                                                                               residue
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90.9%;
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Best Local Similarity
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                                                                                                                                                                                      "Norvalyl carbonyl forming keto-amide linkage with residue 7"
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try useful for treating disorders associated with hepatitis C
             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23
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                                                                                                                                                         'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                     note= "D-form residue"
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                                                                                                                            Key
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Norvalyl carbonyl forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                              sequence represents a peptide compound of the invention having
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Pred. No. 0.026;
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90.9%;
            21-JUL-2000; 2000US-220101P.
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Best Local Similarity 90.9
Watches 10; Conservative
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                                              (CORV-) CORVAS INT INC
                                                                               Levy OE,
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Pred. No. 0.026;
0; Mismatches 1; Indels
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11
/note= "C-terminal amide"
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90.9%;
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                                                                                                                                                                                CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                 virus protease
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hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
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residue 7"
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                                                                                                                                                                     Length 11;
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Pred. No. 0.026;
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90.9%;
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residue 7"
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                                         ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C tease -
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virucide.
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Pred. No. 0.026;
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90.9%;
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                 WPI; 2002-361643/39
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                                                                                                                                                                                                                                                                                                             Sequence
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Search completed: December 22, 2003, 17:41:01 Job time : 32.4667 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                          /note= "Norvaly1 carbony1 forming keto-amide linkage with
residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                              Gaps
                                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.
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Score 46; DB 23; Length 11;
Pred. No. 0.026;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                note= "N-terminal acetyl"
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/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                    ABB80551 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 65; 69pp; English.
 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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                                                                      1 EEVVPXGMDYS 11
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Best Local Similarity
Matches 10; Conserv
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REVVPXGMDYS 11

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Conservative
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; ORGANISM: Citrus unshiu
US-08-853-948B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 VIPPGMDFS 236
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Best Local Similarity
Matches 6; Conserv
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Sequence 8, ...
Sequence 8, Applace Sequence 26805, A
Sequence 4, Appli
Sequence 6, Appli
Company Company
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Sequence 82, Appl
Sequence 31637, A
Sequence 14, Appl
Sequence 8, Appli
Sequence 8, Appli
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                        December 22, 2003, 16:37:03 ; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
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Sequence 11, 1
Sequence 9, Al
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Sequence 10,
Sequence 11,
Sequence 7, A
Sequence 7, A
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Sequence 4, 1
Sequence 4, 1
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Compugen Ltd.
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US-09-853-948B-5
US-09-697-367-24
US-09-394-272-10
US-08-429-054A-11
US-09-394-272-4
US-09-252-991A-31637
US-08-965-313-4
US-09-252-991A-26805
US-09-267-313-4
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                328717 segs, 42310858 residues
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GenCore version (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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54
1 EEVVPXGMDYS 11
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No.
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28 32 59.3 173 1 US-08-193-977-7 Sequence 7, Appliance 29.3 189 2 US-08-464-517-21 Sequence 21, Appliance 22, Appliance 21, Appliance 22, Appliance 21, Appl
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## ALIGNMENTS

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US-08-95-9489-4

Sequence 4, Application US/08851948B

PREFUT. No. 621043

SEQUENCE 4, Application US/08851948B

SEQUENCE 4, Application US/08851948B

SEQUENCE 4, Application US/08851948B

TITLE 0F INVENTION: THE SAME

TITLE OF INVENTION: THE SAME

TOTREE REPRESE PATH OATE: 199-0-5-09

SOFTWARE: PATH OATE: 199-0-5-09

SOFTWARE: PATH OATE: 199-0-5-09

SOFTWARE: PATH OATE: 199-0-5-09

SOFTWARE: PATH OATE: THE SAME

COTHER INPORMATION: PRO, Set, Thr, Trp, Tyr, or Val.

OTHER INPORMATION: PRO, Set, Thr, Trp, Tyr, or Val.

OTHER INPORMATION: PRO, Set, Thr, Trp, Tyr, or Val.

OTHER INPORMATION: PRO, Set, Thr, Trp, Tyr, or Val.

ONE-08-953-948B-4

Beet Local Similarity 66.74; Pred. No. 18; Indels 0; Gaps 0; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Matches 0; Matches 2; Mismatches 2; Mismatches 3; Matches 2; Mismatches 3; Mismatc
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Sequence 7, Application US/08718777
Patent No. 5981852
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
TENGTH: 1068
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Matches 6; Conservative
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MOLECULE TYPE: Peptide
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STRANDEDNESS: Si
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US-08-718-777-7
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Sequence 10, Application US/09394272

Sequence 10, Application US/09394272

Sequence 10, Application US/09394272

Sequence 10, Application US/09394272

APPLICANT: Haigler, Candace H.

APPLICANT: Haigler, Candace H.

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

FILE REFERENCE: 201304/1000

CURRENT APPLICATION NUMBER: US/09/394,272

CURRENT FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.0
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Score 36; DB 3; Length 348;
Pred. No. 19;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                          | Sequence 24, Application US/09697367 |
| Sequence 24, Application US/09697367 |
| Patent No. 6323015 |
| GENERAL INFORMATION: | APPLICANT: | Coraco Jr., Emil M. |
| APPLICANT: | Coraco Jr., Emil M. |
| APPLICANT: | Coraco Jr., Emil M. |
| APPLICANT: | Tarczynski, Mitchell |
| TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE |
| TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE |
| TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE |
| CURRENT APPLICATION NUMBER: US/09/697,367 |
| CURRENT FILING DATE: 1998-MAY-07 |
| PRIOR PELLORATION NUMBER: PCT/US99/09865 |
| PRIOR FILING DATE: 1998-MAY-06 |
| NUMBER OF SEQ ID NOS: 24 |
| SOFTWARE: | Microsoft Office 97 |
| PRIOR FILING DATE: | PRIOR PRI
       66.7%;
66.7%;
Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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217 VIPPGMDFS 225
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234 VIPPGMDFS 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT CORGANISM: Zea mays US-09-697-367-24
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LENGTH: 1049
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Sequence 11, Application US/08429054A

Sequence 11, Application US/08429054A

Sequence 11, Application US/08429054A

Sequence 11, Application US/08429054A

GENERAL INFORMATION:
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: JEAN; VOELKER, TONI; GERVALS, MONICA
ITILE OF INVENTION: CONA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERNAN AND MUSERLIAN
STREET: 6.00 THIRD AVENUE
CITY: NEW YORK
STATES: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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APPLICANT: Lando, D.
APPLICANT: Bruneau, J. M.
APPLICANT: Bruneau, J. M.
APPLICANT: Gervais, M.
TITLE OF INVENTION: MODIFICATION OF SUCROSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPER: FLODEY DISK
MEDIUM TYPER: FLODEY DISK
COMPUTER: IBW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA: 6.6AF-1995
CLASSIFICATION DATA: 05.4AF-1995
CLASSIFICATION DATA: 800
PRIOR APPLICATION DATA: WE 842,337
FILING DATE: 20.AMECH-1992
APPLICATION NUMBER: US 842,337
FILING DATE: 18.July-1991
CLASSIFICATION NUMBER: FCT/FR 91/00593
FILING DATE: 18.July-1991
CLASSIFICATION NUMBER: French 90402094.9
FILING DATE: 20.July-1990
CLASSIFICATION NUMBER: French 90402094.9
FILING DATE: 20.July-1990
CLASSIFICATION NUMBER: 146.1137
TELEFORMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 146.1137
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMEY (21.0.000)
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US-09-394-272-8

| Sequence 8, Application US/09394272 |
| Sequence 8, Application US/09394272 |
| Patent No. 647258 |
| GENERAL INFORMATION: |
| APPLICANT: Haigler, Candace H. |
| APPLICANT: Holaday, A. SCOCT |
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE |
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE |
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE |
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE |
| TITLE OF INVENTION NUMBER: US/09/394,272 |
| CURRENT FILING DATE: 1999-09-10 |
| SUPPRESSION OF SEQ ID NOS: 14 |
| SOFTHAMER OF SEQ ID NOS: 14 |
| SOFTHAMER PATENTIN Ver. 2.0 |
| LENGTH: 1068 |
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Batent No. 6472588

GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REPERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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          FILING DATE: 25-OCT-1996

APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-OCT-1995

PRIOR APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-OM-1995

APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-OM-1995

ATTORNEY/AGENT INFORMATION:
NAME: BALBARA Rae-Vencer. Ph.D., REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: 32,750

TELEPHONE: (415)328-4400

TELEPHONE: (415)328-4400

TELEPHONE: (415)328-4477

INFORMATION FOR SEG ID NO: 7:
SEGUENCE CHARACTERISTICS:
LENGTH: 1068 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-051-341-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 VIPPGMDFS 443
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US-09-394-272-8
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US-09-394-272-4
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Sequence 7, Application US/09051341

Fatent No. 6124528

GENERAL INFORMATION:

APPLICANT: Shewmaker, C. K.

TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE

TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE

TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rae-Venter Law Group, P.C.

STATE: California

COMPTY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopyy disk

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/051,341

FILING DATE:

APPLICATION NUMBER: US/09/051,341
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TITLE OF INVENTION: PHOSPHATE
TITLE OF INVENTION: SYNTHASE IN PLANTS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Barbara Rae-Venter
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777
FILING DATE: NOT YET ASSIGNED
CLASSIFICATION NUMBER: US 08/175,471
FILING DATE: US 08/175,471
FILING DATE: Z-DEC-1993
ATTORNEY/AGERT INPERMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Barbara Rae-Venter
REGISTRATION UNMBER: 32,750
REFERENCE/DOCKET NUMBER: GGNE.072.02US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/US96/17351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415)328-4400
TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1068 amino acids TYPE: amino acid
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Best Local Similarity 66.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-777-7
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CITY: Phi
STATE: PA
COUNTRY:
                           US-08-569-147-76
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APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCORNATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, Candace H.
APPLICANT: Haigler, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET: 2.0
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                                                                                                                             Score 36; DB 4; Length 1081;
Pred. No. 69;
2; Mismatches 1; Indels
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66.7%; Pred. No. 69;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 66.7%; Score 36; DB 4; Length 1083; Best Local Similarity 66.7%; Pred. No. 69; Matches 6; Conservative 2; Mismatches 1; Indels
                                                TYPE: PRT ORGANISM: Craterostigma plantagineum
                                                                                                                                                                                                                                                                                                                                US-09-394-272-11
; Sequence 11, Application US/09394272
; Patent No. 6472588
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US-09-394-272-9
; Sequence 9, Application US/09394272
; Patent No. 6472588
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; ORGANISM: Arabidopsis thaliana
US-09-394-272-11
                                                                                                                             Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Oryza sativa
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LENGTH: 1083
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LENGTH: 1084
SEQ ID NO 4
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Sequence 16, Application US/0859147

PREMEMAL INFORMATION:
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Sequence 31637, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ 1D NO 31637
LENGTH: 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.0%; Score 34; DB 3; Length 140; Best Local Similarity 75.0%; Pred. No. 16; Matches 6; Conservative 0; Mismatches 2; Indels
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Sequence 14, Application US/08963851

Patent No. 6300116

GENERAL INFORMATION:
APPLICANT: HALKIER, TORDEN
APPLICANT: HALKIER, TORDEN
APPLICANT: BAUDITZ, PETER
APPLICANT: BAUDITZ, PETER
APPLICANT: BAUDITZ, PETER
APPLICANT: HANSEN, PETER KAMP
ITLE OF INVENTION: PETER KAMP
CURRENT APPLICATION NUMBER: US/08/963,851

CURRENT APPLICATION NUMBER: US/08/963,851

CURRENT FILING DATE: 1997-11-04

NUMBER OF SOG ID NOS: 35

SOGTAMER PERSER FARESE FOR WINDOWS VERSION 3.0
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILIO, DOTEON TRUJILO, DOTEON TRUJILO, DOTEON TRUJILO, DOTEON TRUJILO, DOTEON TRUJILO, DOTEON TRUJILO, TRUJI
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-82
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US-09-252-991A-31637
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| TYPE: PRT | 1 TYPE: PRT | 1
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CRGANISM: Pinus radiata US-10-393-840-946
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23 VIPPGMDFS 31
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US-10-289-757-73
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ORGANISM:
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Sequence 168, App
Sequence 10, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 4, Appli
Sequence 11, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 1660, Ap
Sequence 58, Appl
Sequence 58, Appl
Sequence 4, Appli
Sequence 4, Appli
                                                                                                  December 22, 2003, 16:40:14; Search time 20.8667 Seconds (without alignments) 98.451 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCCMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NBW_PUB_pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NBW_PUB_pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NBW_PUB_pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB_pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCCMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCCMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCCMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US108_PUBCCMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US108_PUBCCMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US108_PUBCCMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US108_PUBCCMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US108_PUBCCMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCCMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCCMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-10-289-757-73
5 US-10-289-757-16
8 US-10-289-757-10
5 US-10-289-757-71
5 US-10-217-700-8
6 US-10-217-700-8
7 US-10-217-700-9
1 US-09-813-408-27
1 US-09-813-408-27
2 US-10-039-120-4
1 US-09-815-42-5111
2 US-10-029-120-4
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                                                                                                                                                                                                                                                                                              696363 seqs, 186758610 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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54
1 BEVVPXGMDYS 11
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Match Length
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US-10-339-840-946

J Sequence 946, Application US/10393840

J Sequence 946, Application US/10393840

J Sequence 946, Application US. US20030229922A1

J GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
TITLE OF INVENTION: Modification of Plant Cell Wall Polysaccharides

J TITLE OF INVENTION: Modification of Plant Cell Wall Polysaccharides

J TITLE OF INVENTION: Modification of Plant Cell Wall Polysaccharides

J CURRENT APPLICATION NUMBER: US 09/636,800

PRIOR APPLICATION NUMBER: US 09/636,800

PRIOR PELING DATE: 1999-10-13

PRIOR PELING DATE: 1999-10-14

PRIOR PELING DATE: 1999-10-13

PRIOR PELING DATE: 1999-
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US-10-217-700-10

| Sequence 10, Application US/10217700
| Fublication No. US20030070191A1
| Publication No. US20030070191A1
| GENERAL INFORMATION:
| APPLICANT: Helgler, Candace H. |
| APPLICANT: Holday, A. Scott |
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE |
| TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE |
| TITLE REPERENCE: 201304/1000 |
| CURRENT APPLICANTON NUMBER: US/10/217,700 |
| CURRENT APPLICANTON NUMBER: 09/394,272 |
| RARLIER PILING DATE: 1999-09-10 |
| NUMBER OF SEQ ID NOS: 14 |
| SOFTWARE: PatentIN Ver. 2.0 |
| SEQ ID NO 10 |
| LENGTH: 1049 |
| TYPE: PRT |
| ORGANISM: Organ sativa
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Pred. No. 1.5e+02;
2; Mismatches 1; Indels n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 15; Length 1049;
Pred. No. 1.5e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Denmer, Jeroen
APPLICANT: Porster, Richard L
APPLICANT: Glason, John Bryan
APPLICANT: Glason, John Bryan
APPLICANT: Glason, John Bryan
APPLICANT: Glason, Matched Andrew
APPLICANT: No. US20030180751Alriss, Geoffrey
APPLICANT: All Matchew
APPLICANT: All Glann, Matthew
APPLICANT: Hall, Claire
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Compositions isolated from forage
FILE REFERENCE: 11000.1661U
CURRENT APPLICATION NUMBER: US/10/289,757
CURRENT FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOSTWARE PERSENCE OF WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 71, Application US/10289757 Publication No. US20030180751A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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LENGTH: 1062
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Pred. No. 1.3e+02;
2; Mismatches 1; Indels
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                                                                                                      APPLICANT: Commer. Varions APPLICANT: Commer. Varions APPLICANT: Commer. Varions APPLICANT: Gloson, John Bryan
APPLICANT: Shenk, Michael Andrew
APPLICANT: Shenk, Michael Andrew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Hall, Claire
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Grasses and methods for their use
FILE REPERBUE: 11000.1061U
CURRENT APPLICATION NUMBER: US/10/289,757
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/337,703
PRIOR APPLICATION NUMBER: 60/337,703
PRIOR PILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Denmer, Jeroen
APPLICANT: Forster, Richard L
APPLICANT: Gibson, John Bryan
APPLICANT: Gibson, John Bryan
APPLICANT: Shenk, Michael Andrew
APPLICANT: Saulsbury, Keith Martin
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Grases and methods for their use
FILE REFERENCE: 11000.1661U
CURRENT APPLICATION NUMBER: US/10/289,757
CURRENT FILING DATE: 2001-11-07
PRIOR PILLING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOFTWARE FREUSE FREUSE FOR Windows Version 4.0
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Publication No. US20030180751A1
          Sequence 73, Application US/10289757
Publication No. US20030180751A1
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Best Local Similarity 66.7%;
Matches 6; Conservative
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US-10-289-757-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Lolium perenne
US-10-289-757-73
                                                                                         APPLICANT: Demmer, Jeroen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:| |||:|
462 VIPPGMDFS 470
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 938
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RESULT 4

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TYPE: PRT; ORGANISM: Arabidopsis thaliana US-10-217-700-11
                    LENGTH: 1083
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Sequence 11, Application US/10217700

Publication No. US20030070191A1

GENERAL INFORMATION:
APPLICANT: Haigler, Candace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION WIMBER: US/10/217,700
CURRENT FPLICATION NUMBER: US/10/217,700
CURRENT FILING DATE: 1999-09-10
EARLIER APPLICATION UNMBER: US/394,272
EARLIER FILING DATE: 1999-09-10
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10217700
| Publication No. US20030070191A1
| GENERAL INFORMATION:
| APPLICANT: Haigler, Candace H.
| APPLICANT: Haigler, Candace H.
| TITLE OF INVENTION: EXPRESENCE FIBER PRODUCING PLANTS WITH INCREASED
| TITLE OF INVENTION: EXPRESENCE FIBER PRODUCING PLANTS WITH INCREASED
| TITLE OF INVENTION: EXPRESENCE 20134/1000
| CURRENT PRILICATION NUMBER: US/10/217,700
| CURRENT FILING DATE: 1999-09-10
| BARLIER PLING DATE: 1999-09-10
| WUMBER OF SEQ ID NOS: 14
| SOFTWARE PLANTS OF SECTION OF SE
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APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700
CURRENT FILING DATE: 2002-08-12
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VOY: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Craterostigma plantagineum
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 VIPPGMDFS 443
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; ORGANISM: Zea mays
US-10-217-700-8
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LENGTH: 1081
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Sequence 27, Application US/09813408
| Publication No. US20030049619A1 |
| GRNERAL INFORMATION: |
| GRNERAL INFORMATION: |
| APPLICANT: Delagrave, Simon |
| APPLICANT: Marrs, Barry |
| TITLE OF INVENTION: Methods For The Synthesis Of Polynucleotides And Combinatorial |
| TITLE OF INVENTION: Of Polynucleotides |
| TITLE OF INVENTION: OF POLYNUCLEOTICE |
| TITLE OF INVENTION: OF POLYNUCLE |
| TITLE
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Publication No. US20030070191A1

Publication No. US20030070191A1

GENERAL INFORMATION:

APPLICANT: Haigler, Candace H.

APPLICANT: Holdedy, A. Scott

TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE

TITLE OF INVENTION WHEER: US/10/217,700

TITLE APPLICATION NUMBER: 09/394,272

RARLIER PILING DATE: 1999-09-10

MUMBER OF SEQ ID NOS: 14

SOFTWARE PATENTIN UST: 2.0
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        Length 1083;
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Pred. No. 92;
2; Mismatches 1; Indels
                                                                                  1; Indels
Query Match 66.7%; Score 36; DB 15; Best Local Similarity 66.7%; Pred. No. 1.6e+02; Matches 6; Conservative 2; Mismatches 1;
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66.7%;
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66.7%;
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Best Local Similarity 66.70,
6; Conservative
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; TYPB: PRT
; ORGANISM: Aeropyrum pernix
US-09-813-408-27
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Best Local Similarity 66.7
Matches 6; Conservative
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453 VIPPGMDFS 461
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483 VIPPGMDFS 491
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VVPXGMDYS 11
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Gaps

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Sequence 4, Application US/10029120

Sequence 4, Application US/10029120

Publication No. US20030175708A1

GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
ITIME OF INVENTION: UUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/029,120
CURRENT PILING DATE: EALIER FILING DATE: 1999-09-29
FRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
SROOF OF SEQ ID NOS: 123
SOFTWARE: FASELSEQ for Windows Version 3.0
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  Indels
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APPLICANT: Mall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yumamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLB OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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85.7%; Pred. No. 3.9e+02;
iive 0; Mismatches 1;
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PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PARESEQ for Windows Version 4.0
SERIGTH: 1062
Mismatches
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                             Sequence 5111, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
5, Conservative
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                                             1 REVVPXGMDY 10
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HICH, YOUR
APPLICANT: NAGAI, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: SOSHIKANA, TSUTOMU
APPLICANT: OYSUKA, MOTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE REFERENCE: 048.335/0160
CURRENT APPLICATION NUMBER: 2002-03-12
FRIOR APPLICATION NUMBER: 60/350,435
FRIOR APPLICATION NUMBER: 60/350,435
FRIOR APPLICATION NUMBER: 202-03-12
FRIOR APPLICATION NUMBER: 10 2001-0324
FRIOR PILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
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Sequence 58, Application US/10091007

Publication No. US2003017078241

Sequence 58, Application US/10091007

Publication No. US2003017078241

APPLICANT: Harniffy

APPLICANT: Hanniffy

APPLICANT: Hanniffy

TITLE OF INVENTION: Proteins

FILE REFRENCE: PWCP2197000

CURRENT APPLICATION NUMBER: US/10/091,007

CURRENT FILING DATE: 2002-0-06

PRIOR FILING DATE: 1999-09-07

NUMBER OF SEQ ID NOS: 276

SOFTWARE: Patentin version 3.0

SEQ ID NO 58

LENGTH: 222
                                                                 Sequence 1660, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
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; ORGANISM: Streptococcus agalactiae
US-10-091-007-58
                                                                                                                                        APPLICANT: ISOGAL, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHIJ, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity
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Gaps

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US-10-027-806-4

i Sequence 4, Application US/10027806

j Publication No. US2020160476A1

j GENERAL INFORMATION:

APPLICANT: Swanson, Ronald V.

APPLICANT: Schlaper, Christa

TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM

TITLE OF INVENTION: NUMBER: US/10/027,806

CURRENT FAPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020

PRIOR PLING DATE: EARLIER FILING DATE: 1999-09-29

PRIOR PLING DATE: EARLIER FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FRALES FILING DATE: ALTER FILING DATE: 1999-09-29

SOFTWARE: PAT

LENGTH: 3472

TYPE: PRT

ORGANISM: Cenarchaeum symbiosum

US-10-027-806-4
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                                                                                                                     Query Match 63.0%; Score 34; DB 12; Length 3472; Best Local Similarity 45.5%; Pred. No. 1.5e+03; Matches 5; Conservative 4; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.0%; Score 34; DB 14; Length 3472; Best Local Similarity 45.5%; Pred. No. 1.5e+03; Matches 5; Conservative 4; Mismatches 2; Indel8 (
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; LENGTH: 3472
; TYPE: PRY
: ORGANISM: Cenarchaeum symbiosum
US-10-029-120-4
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2294 EDVIPRGISFS 2304
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2294 EDVIPRGISFS 2304
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GenCore version 5.1.6
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- protein search, using sw model OM protein

December 22, 2003, 17:24:36; Search time 9.06667 Seconds (without alignments) 116.675 Million cell updates/sec Run on:

US-09-909-164-13 54 1 BEVVPXGMDYS 11 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	conserved hypothet	V1 protein - tobac	sucrose-phosphate	sucrose-phosphate	unknown protein F2	sucrose-phosphate	sucrose-phosphate	sucrose-phosphate	вистове-phosphate	sucrose-phosphate	hypothetical prote	peptidoglycan-bind	probable alkaline	hypothetical prote	probable membrane	fat facets (faf) s	plastocyanin b - L	plastocyanin precu	plastocyanin b pre	6-0-methylguanine-	O6-methylguanine-D	hypothetical prote	probable hexosyltr	L-lactate dehydrog	ABC transporter AT	phenylalanine-tRNA	succinate dehydrog	disease resistance
SUMMARIES	ID	854619	D69551	A42452	S72649	S72650	G96764	JC4783	JQ1329	T09837	T04062	T04103	T24111	H87660	H72784	T20173	F69009	B49132	800210	S38255	S58208	AG3104	D98182	F72745	G69290	G69350	E86665	A70164	F81138	T48898
	DB	7	N	N	N	~	N	N	-	N	7	N	N	~	~	~	~	N	N	N	N	N	~	~	-	~	~	~	~	7
	Query Match Length	156	363	102	341	348	460	1049	1068	1081	1083	1084	425	433	440	1150	1474	2747	66	155	168	290	290	296	357	366	265	266	587	906
de	Query	74.1	70.4	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	64.8	64.8		64.8	64.8	64.8	m	m	63.0	63.0	63.0	63.0	n	63.0	63.0	63.0	63.0	63.0
	Score	40	38	36	36	36	36	36	36	36	36	36	35	35	32	32	35	35	34	34	34	34	34	34	34	34	34	34	34	34
	Result No.	-	7	m	4	S	φ	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

disease resistance RND multidrug effi hypothetical prote hypothetical 367K partial transposas hypothetical prote fibroblast growth hypothetical prote conserved hypothet unknown protein [1 transposase ISC105 transposase ISC105	hypothetical prote pantoate-beta-alan transposase ISC105
748899 733830 733830 733830 73383 7338 73427 73621 736	C64417 G83055 B90487
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908 1062 1062 3472 97 128 172 184 225 225 247 267	276 283 299
633.0 633.0 611.1 611.1 611.1 611.1	61.1 61.1 61.1
4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 8 8 8 8 8 8 8 8
	4 4 4 6 4 0

# ALIGNMENTS

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hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein 02612; hypothetical protein YOL303.3
C;Species Saccharomyces cerevisiae
C;Date: 0e-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 19-Apr-2002
C;Accession: 654619; S66879
R;de Haan, M.; Maarse, A.C.; Grivell, L.A.
R;Accession: 654619; A.C.; Grivell, L.A.
R;Accession: 854617
A;Reference number: S54617
A;Recence number: S54617
A;Recence number: S54617
A;Recence cures: Saccious A;Recence cures: Saccious A;Recence cures: Saccious A;Recence cures: Saccious A;Recence number: S6419
A;Recence number: S6419
A;Recence number: S6879
A;Recence number: S68877
A;Recence number: S66879
A;Recence number: S68877
A;Recence number: S66879
A;Recence number: S66879
A;Recence number: S68877
A;Recence

Gape ö 'Match 74.1%; Score 40; DB 2; Length 156; Local Similarity 77.8%; Pred. No. 1; Conservative 1; Mismatches 1; Indels Query Match Matches

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2 EVVPXGMDY 10 ||:| |||| 50 EVMPLGMDY 58 ò 셤

Conserved hypothetical protein AP2411 - Archaeoglobus fulgidus
Conserved hypothetical protein AP2411 - Archaeoglobus fulgidus
Conserved hypothetical protein AP2411 - Archaeoglobus fulgidus
Conserved hypothetical protein and a conserved hypothetical and a conserved hypothetical and a conserved hypothetical and a conserved hypothetical and a conserved hypothem, A. P. Clayton, R.A. Tomb, J.P.; White, O.; Nelson, G.G.; Gill, S.; Kairkness, B. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.
Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Complete genome sequence of the hyperthermophilic, sulfate-reducing archanaly Reference number: A69250; MuID:98049343; PMID:9389475
A;Accession: D69551
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

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unknown protein F25P22.17 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: G96764
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alons: Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K ansen, N.F.; Hudghes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial.
Rizzo, M.; Rooney, T.; Rowartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A66141; MUID:21016719; PMID:11130712
A; Residues: DNA
A; Residues: L-460 cSTO>
A; Residues: L-460 cSTO>
A; Residues: L-460 cSTO>
A; Cross-references: GB:AE005173; NID:g6692750; PIDN:AAF24856.1; GSPDB:GN00141
          Bucrose-phosphate synthase (BC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
C;Species: Citrus unshiu
C;Species: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: 572650
R;Komateu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Wol. Gen. Genet. 252, 346-351, 1996
A;Title: Cloining and molecular analysis of CDNAs encoding three sucrose phosphate synt:
A;Reference number: 872648; WUID:96439842; PMID:8842155
A;Accession: 572650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructo: A; Pathway: sucrose biosynthesis
C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology
C; Superfamily: sucrose-phosphate synthase; sucrose-phosphate synthase homology
F;1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>
                                                                                                                                                                                                                                                                                                 A.Status: nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 1-348 <KOM>
A.Residues: 1-348 <KOM>
A.Cross-references: EMBL.AB006660; NID:92351059; PIDN:BAA22071.1; PID:92351060
A.Rxperimental source: fruit, cv. Miyagawa-Wase
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Score 36; DB 2; Length 460; 70.0%; Pred. No. 23; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%; Score 36; DB 2; Length 348; 66.7%; Pred. No. 17; ive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 66.7
Matches 6; Conservative
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Matches 7; Conservative
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234 VIPPGMDFS 242
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A,Gene: F25P22.17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virtue tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Spacesion: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yellow A;Recession: A42452
A;Accession: A42452
A;Accession: A42452
A;Accession: DNA
A;Residues: 1-102 < MOR>
A;Residues: 1-102 < MOR>
A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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Mol. Gen. Genet. 252, 346-351, 1996
Apittle: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate syntha
A;Reference number: S72648; MUID:96439842; PMID:8842155
A;Accession: S72649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fructose A; Pathway: sucrose blosynthesis
(S. Superfamaily: sucrose-phosphate synthase; sucrose-phosphate synthase homology C; Keywords: glycosyltransferase; haxosyltransferase; sucrose-blosynthesis
F;1-341/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <8SPS>
A;Molecule type: DNA
A;Residues: 1-363 <KLE>
A;Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068
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A;Residues: 1-341 <KOM>
A;Cross-references: BMBL:AB006319; NID:g2588891; PIDN:BAA23215.1; PID:g2588892
A;Experimental source: fruit, cv. Miyagawa-Wase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
C;Genetics:
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C;Species: Citrus unshiu
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C;Accession: S72649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 16;
2; Mismatches 1; Indels
                                                                                                                                 Length 363;
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Pred. No. 4.3;
3; Mismatches
                                                                                                                                 DB 2;
                                                                                                                                 Score 38; DB;
Pred. No. 6.8;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.7%;
ilarity 66.7%;
Conservative
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ilarity 60.0%;
Conservative 3
                                                                                                                                 Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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7 QVVPSGINYS 16
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Matches 6; Conserv
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nes 6; Conser
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Best Loc Matches

RESULT 4

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Gaps

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RESULT 5

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Bucrose-phosphate synthase homolog F28M11.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
C;Accession: T04062
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F submitted to the Protein Sequence Database, March 1999
A;Accession: T04062
A;Molecule type: DNA
A;Pathway: sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Reymords: gjycosyltransferase; hexosyltransferase; sucrose biosynthesis
P;176-674/Domain: sucrose/sucrose-phosphate synthase homology <SSS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1083 -8EV>
A;Cross-references: EMBL:AL049487
A;Cross-references: EMBL:AL049487
A;Cross-references: EMBL:AL049487
C;Genetics:
A;Map position: 4
A;Intores: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3; A;Note: F28M1.40
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology P;230-714/Domain: sucrose-phosphate synthase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Oryza sativa (rice)
C;Dace: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Dacession: T04103
R;Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T.
Plant Sci. 112, 207-217, 1995
A;Title: Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene
A;Reference number: 215212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
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Pred. No. 60;
2; Mismatches 1; Indels
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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A;Crose-references: EMBL:D45890; PIDN:BAA08304.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: subsp. Japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conservative
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445 VIPPGMDFS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| |||:|
483 VIPPGMDFS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VVPXGMDYS 11
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                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1049 < VAL>
A; Cross-references: GB: 13175; NID: g1449931; PIDN: AAC49379.1; PID: g988270
A; Note: UPEqlucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDEglucosylt
C; Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
C; Genetics:
A; Gene: Sps1
A; Introns: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3; 9
C; Punction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gucrose-phosphate synthase (EC 2.4.1.14) - maize
C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JQ1329; PQ0260
R;Worrell, A.C.; Bruneau, J.M.; Summerfelt, K.; Boersig, M.; Voelker, T.A.
Paint Cell 3, 1121-1130, 1991
A;Title: Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohyd
A;Reference number: JQ1329; MUID:92338837; PMID:1840396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: POOCSO
A;Molecule type: protein
A;Residues: 71-74;206-212;471-481;872-892 <WOR1>
C;Comment: This enzyme transfers the glucosyl group from UDPglucose to fructose-6-phosph C;Comment: This enzyme is involved in the regulation of carbon partitioning in the leave C;Punction:
C;Date: 10-May-1996 #Bequence_revision 16-Aug-1996 #text_change 18-Jun-1999
C;Accession: JC4783
R;Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moraila, B.; Herrera-Estrella Gene 170, 217-222, 1996
A;Title: Characterization of a rice sucrose-phosphate synthase-encoding gene.
A;Reference number: JC4783; MUID:96235138; PMID:8666248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
A;Pathway; sucrose biosynthesis
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; haxosyltransferase; sucrose biosynthesis
F;180-663/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis F;178-666/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Craterostigma plantagineum C;Species: Craterostigma plantagineum C;Species: Craterostigma plantagineum C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C;Accession: T09837 R;Ingram, J.; Chandler, J.W.; Gallagher, L.; Salamini, F.; Bartels, D.
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A;Residues: 1-1068 <WOR>
A;Cross-references: GB:M97550; NID:g168625; PIDN:AAA33513.1; PID:g168626
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Pred. No. 58;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1068;
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Pred. No. 59;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th 66.7%;
Similarity 66.7%;
6; Conservative 5
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Best Local Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436 VIPPGMDFS 444
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Best Local Similarity
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: H72784
R;Kawarabayasi, Y:; Hino, Y:; Horikawa, H:; Yamazaki, S:; Haikawa, Y:; Jin-no, K:; Taki
B;Kawarabayasi, Y:; Hino, Y:; Horikawa, T:; Tanaka, T:; Kudoh, Y:; Yamazaki, J:;
NA Res. 6, 83-101, 1999
A;Rtitle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop;
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: H72784
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-440 «KAW»
A;Coss-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79178.1; PID:g5103657
A;Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C53A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20173; T23857
R;Mortimore, B.
R;Mortimore, Caenore, Caenore, Cort., Caenore, Caenore
                                                                                                                                          probable alkaline proteinase APE0263 - Aeropyrum pernix (strain K1)
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Pred. No. 35;
2; Mismatches
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A;Gene: APE0263
C;Superfamily: subtilisin; subtilisin homology
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Best Local Similarity 66.7%;
Matches 6; Conservative
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562 VLPVGIDYS 570
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                                                                     RESULT 14
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C:Species: Canlobacter crescentus
C:Species: Canlobacter crescentus
C:Species: Canlobacter crescentus
C:Species: Canlobacter crescentus
R:Noierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Gwinn, M.L.; Haft, D.H.; Kolon
N. J.; Brmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; WUID:21173698; PMID:11259647
                                                                     A;Map position: 1
A;Map position: 1
A;Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
C;Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltranaferase; hexosyltranaferase
F;196-680/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
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A;Molecule type: DNA
A;Residues: 1-425 <WILL.
A;Residues: 1-425 <WILL.
A;Cross-references: EMBL:Z81109; PIDN:CAB03241.1; GSPDB:GN00023; CBSP:R10D12.10
A;Experimental source: clone R10D12
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A;Cross-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC3322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                            Length 1084;
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Pred. No. 34;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein R10D12.10 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                            Score 36; DB 2;
Pred. No. 60;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                            66.7%;
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Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.
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Best Local Similarity 50.0
Matches 5; Conservative
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453 VIPPGMDFS 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: CESP:R10D12.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: T24111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 5
C;Genetics:
A;Gene: Sps1
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Gaps

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1; Indels

Length 440;

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A;Map position: 5
A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2; ·
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Rimatthews, L.

submitted to the EMBL Data Library, August 1996

A; Reference number: Z19808

A; Reference number: Z19808

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Rotecule type: DNA

A; Residues: 1-1150 < WIZ>

A; Cross-references: EMBL: Z78015; PIDN: CAB01437.1; GSPDB: GN00023; CESP: C53A5.2

A; Experimental source: clone R02D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1150;
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                                                                                                                                                                                                                                                                                                                                                                                                                64.8%; Score 35; DB 2;
llarity 66.7%; Pred. No. 1e+02;
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 22, 2003, 17:44:58 Job time : 10.0667 secs
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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 22, 2003, 16:43:51; Search time 4.6 Seconds

(without alignments)

112.455 Million cell updates/sec
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Title: US-09-909-164-13
Perfect score: 54
Sequence: 1 EBVVPXGMDYS 11
Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5 Searched: 127863 seqs, 47026705 residues Total number of hits satisfying chosen parameters: 127

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	OBrq86 fusobacteri	-	_		m	P55824 drosophila	4	P20423 oryza sativ	80	_			Q8w4j9 arabidopsis			_	~			Q9zeu7 halomonas e			-	074377 schizosacch	simian	6	2 homo say	P19102 xenopus lae		Q92bc5 listeria in	Q8y6u8 listeria mo	Q04667 rattus norv	P08203 escherichia
ID	CARB FUSIN		SPS ORYSA	SPS_MAIZE	SPSZ CRAPL	PAP DROME	KHL1 HUMAN	PLAS_ORYSA	PLAS HORVU	PLAT POPNI	SYFB_BORBU	R8L4 ARATH	RPP8 ARATH	RP8H ARATH	Y939_METJA	PANC_PSEAE	HMPA_VIBCH	ACDM RAT	BCB2 HALEL	BCB1 HALEL	BCB2 HUMAN	FGR3 MOUSE		SULH SCHPO	ENV SFV3L	RPOC VIBCH	ZEP1 HUMAN		PLAS DAUCA	TPX LISIN		HES3 RAT	ARAD_ECOLI
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& Query Match	70.4	66.7	66.7	66.7	66.7	64.8	63.9		•	63.0	63.0	63.0	63.0	63.0	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1		•	59.3	59.3	59.3	•
Score	38	36	36	36	36	35	34.5			34	34	34	34	34	33	33	33		33	33	33	33	33	33	33	33	33	32.5	32	32	32	32	32
Result No.	-	2	3	4	S	9	7	80	σ	10	11	12	13	14	15	16	17		19	20	21	22	23	24	25	56	27	28	29	30	31	32	

P06190 salmonella Q9wzri thermotoga Q04827 rattus norv P30279 homo sapien P30280 mus musculu Q90459 brachydanio P50755 xenopus lae P53782 xenopus lae P55169 gallus gall P30281 homo sapien P24385 homo sapien
ARAD SALTY HIS9_THEMA CGD2_RAT CGD2_RAT CGD2_RAT CGD1_ROUSE CGD1_REARE CGD1_REARE CGD2_CHICK CGD2_CHICK CGD2_CHICK CGD2_THUMAN CGD3_THUMAN
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# ALIGNMENTS

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TO 3-FEB-2003 (Rel. 41, Lest and the sequence update)

TO 3-FEB-2003 (Rel. 41, Lest and the sequence update)

TO 3-FEB-2003 (Rel. 41, Lest and the sequence update)

TO 3-FEB-2003 (Rel. 41, Lest and the sequence update)

TO 3-FEB-2003 (Rel. 41, Lest and the sequence update)

TO CARDAMOYI-phosphate synthase large chain (EC 6.15.5) (Carbamoyl-Phosphate synthase largeman A. Gardder W. Greckhind (G. Zhul L. Rogan Y. Chaga O. Golfeman E. Bernal A. Shattacharya A. Bartama A. Gardder W. Greckhind R. Zhul L. Kogan Y. Chaga O. Golfeman E. Bernal A. Shattacharya A. Bartama A. Gardder W. Greckhind R. Shattacharya A. Bartama A. Gardder W. Carbamoyl Phosphate (E. Carbamoyl Phosphate C. Carbamoyl Phosphate A. Deglutamate + carbamoyl phosphate (EQ 6.16) (G. Gardder W. Carbamoyl Brosphate (EQ 7.10) (G. Gardder W. Carbamoyl
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PRT; 1049 AA.

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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-Phosphate synthase (BC 2.4.1.14)
(UDP-glucose-fructose-phosphate glucosyltransferase).
                                                                                                                       STANDARD;
                                    7 QVVPSGINYS 16
                                                                                                                                                                                                                                          Oryza sativa (Rice)
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SEQUENCE
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SPS MAIZE
                                                                                      RESULT 3
SPS ORYSA
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AR PEam; PF02142; MGS; 1.

DR PRINTS; PR00098; CPSASE.

DR PROSITE; PS00866; CPSASE.

DR PROSITE; PS00866; CPSASE.; 2.

DR PROSITE; PS00867; CPSASE.; 2.

KW Arginine biosynchesis; Pyrimidine biosynchesis; Ligase; Repeat;

CARBOXYPHOSPHATE SYNTHETIC DOMAIN.

402 546 CARBAMONL PHOSPHATE SYNTHETIC DOMAIN.
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MEDLINE=92188538; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants.";
Virology 187:633-642(1992).
                                                                                                                                                                                                                                                    ATP (POTENTIAL).
352
ATP (POTENTIAL).
284
MANGANESE I (BY SIMILARITY).
298
MANGANESE I AND 2 (BY SIMILARITY).
300
MANGANESE 2 (BY SIMILARITY).
820
MANGANESE 3 (BY SIMILARITY).
831
MANGANESE 3 (BY SIMILARITY).
832
MANGANESE 3 (BY SIMILARITY).
834
117451 MW; ED7037AF77CLE39F CRC64;
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Pred. No. 9.1;
3; Mismatches 1; Indels
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6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobacco yellow dwarf virus (strain Australia) (TYDV).
Viruses, seDNA viruses, Geminiviridae, Mastrevirus.
NCBI_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 AA
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(Rel. 26, Last seq
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Hypothetical 11.2 kDa protein.
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546
1058
210
352
284
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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01-JUL-1993
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P31619;
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                                                                                                                                                                                                                                                                                                                                                                                                           BUCTOBE 6-PROBPHATE.

-I-ENEYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTRATION OF WETABOLITES AND LIGHT.

-I-PATHWAY: Sucrose synthesis.

-I-SUBUNIT: Homodimer or homotetramer (By similarity).

-I-PATHWAY: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).

-I-SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                THE LEAVES OF PLANTS. MAY REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREPORTS PLAY A MAJOR POLLS AS A LIMITING FACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE LEAF.

-1- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                       Herrera-Estrella L.;
"Characterization of a rice sucrose-phosphate synthase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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1049 AA; 116455 MW; ED862E2819AA4B04 CRC64;
STRAIN=CV. Indica-IR36; TISSUB=Leaf;
MEDLINE=96235138; PubMed=8666248;
Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pik; ucaros; disagnation of the property of trans 1.
InterPro; IPR001296; Glyco trans 1.
Pfam; PP00534; Glycos transf_1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
29 POLY-GLY.
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P31927;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U33175; AAC49379.1; -. PIR; JC4783; JC4783.
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698
779
                                                                                                                                                                          gene.";
Gene 170:217-222(1996)
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                                                                                                                                                                                                                                                                                                                                                                          BUCKOBE 6-PROSPHATE.

-I-ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTRATION OF WETABOLITES AND LIGHT.

-I-PATHWAY: SUCYOSE SYNTHESIS.

-I-SUBUNIT: HOMODIMET OF HOMOCETTAMET (By similarity).

-I-THM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).

-I-SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                        Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D.;
"Analysis of cDNA clones encoding sucrose-phosphate synthase in
relation to sugar interconversions associated with dehydration in the
resurrection plant Craterostigma plantagineum Hochst.";
Plant Physiol. 115:113-121(1997).
-!- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
THEREPORE PLAY A MAJON ROLE AS A LIMITING FACTOR IN THE EXPORT OF
PHOTOASSIMILATES OUT OF THE LEAF.
-!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P55824; Q9V976; Q7V027;
01-NOV-1997 (Rel. 35, Created)
28-F8B-2003 (Rel. 35, Created)
28-F8B-2003 (Rel. 41, Last sequence update)
28-F8B-2003 (Rel. 41, Last sequence update)
Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)
Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)
Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)
Probable ubiquiting enzyme FAF) (Ubiquitin-specific processing protease FAF) (Explain carboxyl-terminal hydrolase FAF)
PAF) (Boubiquitinating enzyme FAF) (Fat facets protein).
PAF) Robbitina melanogaster (Fruit fly).
Bricaryota, Metazzoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bohydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asteridae; lamiids; Lamiales; Lamiales incertae sedis; Torenieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 36; DB 1; Length 1081; 66.7%; Pred. No. 24; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1081 AA; 120933 MW; DD142DC2F1A72900 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fischer-Vize J.A., Rubin G.M., Lehmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ARG
                                                                                            SEQUENCE FROM N.A.
MEDLINE-97451773; Pubmed-9306694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Bye imaginal disk;
MEDLINE=93202020; Pubmed=1295747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y11795; CAA72491.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 66.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264
790
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445 VIPPGMDFS 453
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                                                NCBI TaxID-4153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. PIONEER 3184; TISSUE=Leaf;
MEDLINE=92338837; PubMed=1840396;
Worrell A.C., Bruneau J.-M., Summerfelt K., Boersig M., Voelker T.A.;
"Expression of a maize sucrose phosphate synthase in tomato alters
leaf carbohydrate partitioning.";
Plant Cell 3:1121-1130(1991).
-!- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
THEREFORE PLAY A MAJOR ROLLE AS A LIMITING FACTOR IN THE EXPORT OF
PHOTOASSIMILATES OUT OF THE LEAF.
-!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craterostigma plantagineum.
Eukaryota: Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose-phosphate grucosyltransferase 2)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-
                                                                                                                                                                                                                                                             SEQUENCE PROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENZYME FUNCTION.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 1; Length 1068;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR001296; Glyco trans 1.
Pfam; PF00534; Glycos transf 1; 1.
Transferase; Glycosyltransferase; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1081 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-GLY
                                                                         phosphate glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M97550; AAA33513.1; -. PIR; JQ1329; JQ1329.
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                                                                                                                                                                                                            NCBI_TaxID=4577;
                                                                                                                       Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MaizeDB; 25294;
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Matches

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Gaps

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COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR

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RA Adams M.D., Celnighers S.E., Lip P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,
B. Amanatides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,
B. Sutton G.G., Worthas J.E., Richards S. Ashburner M., Henderson S.N.,
B. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champpe M., Fefeiffer B.D.,
R. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champpe M., Fefeiffer B.D.,
R. Ballew R.M. Basu A., An H.-J., Andrews-Feankoch C., Baldwin D.,
B. Ballew R.W. Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.W. Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.W., Bouch E.B., Downes M., Uadrews-Feankoch C., Buldwin D.,
R. Burtis R.C., Busam D.A., Buller H., Cadeu E., Center A., Chandra I.,
R. Burtis R.C., Busam D.A., Buller H. W., Cadeus F., Chandra I.,
R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
R. Andris M.L., Harvey D., Heiman T.J., Herrandez J.R., Harris M.L.,
R. Harris M.L., Harvey D., Heiman T.J., Herrandez J.R., Harris M.L.,
R. Hostin D., Housen K.A., Helman T.J., Herrandez J.R., Retchum K.A.,
Alush F., Karpen G.H., Kez J.C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Matterd B., McIntcoh T.C., McLeodo M.P., McBharson D.,
Merkulov G., Milshina M.V., Mobarry C., Morris J., McBharson D.,
Reson K., Moy M., Murphy B., Murphy L., Murshy D., Puri V., Reele M. A.,
Shue B.C., Siden-Kamos I., Simpson M., Strong R., Shu H.,
Shier E., Spradling A.C., Stapleton M., Strong R., Shu B.,
Syirekas R., Moodey T., Worker E., Wu D., Yang G., Zhan G., Shen H.,
Shier E., Saden-Kamos I., Simpson M., Strong R., Shu B.,
Syirekas R., Worse E.W., Rubing C.W., Wu D., Yang G., Zhan Y., Shih H.,
R. Hang C.-Y., Wassarman D.A., Weiler E., Wu D., Yang G., Shih H.,
Shier E., Spradling A.C., Stapleton M., Shue B.C., Stapleton W., Shue B.C., Stap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: REQUIRED FOR EYE AND EMBRYO DEVELOPMENT, AND PLAYS A ROLE IN COMPOUND EYE ASSEMBLY AND COGENESIS RESPECTIVELY. IN THE LARVAL EYE DISKS, CELLS OUTSIDE THE ASSEMBLING FACETS REQUIRE THIS PROFILE FOR SHORT-RANGE CELL INTERACTIONS THAT PREVENT THE MYSTERY CELLS FROM BECOMING PHOTORECEPTORS. IT IS ALSO REQUIRED FOR NUCLEAR MIGRATION AND CELLULARIZATION IN EARLY EMBRYOGENESIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Annotation of the Drosophila melanogaster euchromatic genome: a
The fat facets gene is required for Drosophila eye and embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
MEDLINE=20196012; PubMed=10731138;
MEDLINE=20196012; PubMed=10731138;
Stablaton M., Hory D.A.;
Stapleton M., Harvey D.A.;
"A Drosophila complementary DNA resource.";
Science 287:2222-2224(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1089-2778 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley;
MEDLINE=22426069; PubMed=12537572;
                                                                                                                         STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                Development 116:985-1000(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  systematic review.";
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GO; GO:0007349; C:Cytoplasm; IDA.
GO; GO:0007349; P:cellularization; IMP.
GO; GO:0007349; P:cellularization; IMP.
GO; GO:0009795; P:embryonic morphogenesis; IMP.
GO; GO:0000979; P:muclear migration; IMP.
GO; GO:000097; P:nuclear migration; IMP.
InterPro; IPR001394; UCH-2.
InterPro; IPR001394; UCH-2.
ProsiTTS; PS00972; UCH-2.
PROSITTS; PS00973; UCH-2.3; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V; Hydrolase, Thiol protesse;
Vision; Alternative splicing.
BY SIMILARIY.
BY SIMILARITY.
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KCRALITY.
AY SIMILARITY.
ATLEPAGMSELTTWEKNISOENPQAKSSLO. -> VTRA
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                                                                                                                                                                               Isoid=PS5824-3; Sequence=VSP 005269;
TISSUE SPECIFICITY: EYE DISKS AND OVARIES.
DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
SIMILARITY: Belongs to peptidase family C19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IATAATLEPAGMSELTTMVEKNLIISQENPQAKSSLQ
SQRQQL (in 1soform 2).
              FUNCTION.

CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0
                                                           Bvent=Alternative splicing; Named isoforms=1;
Comment=Experimental confirmation may be lacking for some
isoforms;
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T -> S (IN REF. 1; AAF01345)
MW; FFB90438BA53A02B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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/FTId=VSP_005269.
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Pred. No. 1.1e+02;
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                                                                                                                                                      IsoId=P55824-2; Sequence=VSP_005270;
                                                                                                                           IsoId=P55824-1; Sequence=Displayed;
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2725 2725
2778 AA; 311139
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54.5%;
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Best Local Similarity 54.5.,
6; Conservative
                                        ubiquitin + a thiol.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al protein;
1677 1677
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ACT SITE 1677
ACT SITE 1976
ACT SITE 1976
VARSPLIC 2705
                                                                                                               Name=1;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=20277482; PubMed=10819331;
Magase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XVII.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF
THE BRAIN CELLS.
                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20347694; PubMed=10888605;
Koob M.D., Nemes J.P., Benzow K.A.,
"The SCAS transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KLHLI).";
Hum. Mol. Genet. 9:1543-1551 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C11C43D8282F9FF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIBCELLUIAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Highly expressed in brain.
-!- SIMILARITY: Contains 1 BTB/POZ domain.
-!- SIMILARITY: Contains 6 Kelch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kelch repeat; Repeat. SER-RICH.
              09NR64; 09H4X4; 09NR65; 09P238;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
KLHLI OR KIAA1490.
Homo sapieng (Human)
  748 AA
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KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
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EMBL, AF252279; AAF81716.1; -.
EMBL, AB040923; BAA96014.1; ALT_INIT.
EMBL, AL353738; CAC16128.1; -.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00651; BTB; 1.
Pfam; PF01344; Kelch; 6.
SMART; SM00225; BTB; 1.
SMART; SM0612; Kelch; 6.
PROSITE; PS50097; BTB; 1.
Cytoskeleton; Actin-binding; Ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82680 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 179-409 FROM N.A.
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:6352; KLHL1.
MIM; 605332; -.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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  KHL1 HUMAN
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SEQUENCE
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REPEAT
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DB 1; Length 748;

Score 34.5;

63.9%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee J.-8.; "Molecular cloning and characterization of plastocyanin precursor in
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Bhrhartoideae; Oryzeae; Oryza.
KBr Dartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BTRAIN=CV. Japonica;
MEDLINE=89386623; PubMed=2780537;
Yano H., Kamo M., Tsugita A., Aso K., Nozu Y.;
The amino acid sequence of plastocyanin from rice (Oryza sativa, subspecies japonica).";
Protein Seq. Data Anal. 2:385-389 (1989).
I- FUNCTION: Participates in electron transfer between P700 and tytochrome b6-f complex in photosystem I.
-:- SUBCELGUAR LOCATION: LOCSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURPACE IN CHLOROPLASTS.
-:- SIMILARITY: Contains 1 plastocyanin-like domain.
                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; P20423; ...
InterPro; IPR000923; BlueCu 1.
InterPro; IPR001235; Copper blue.
Pfam; PR0012; copper-bind; 1.
ProDom; PR00125; Copper-blue; 1.
PROSITE; PS00196; COPPERBLUE.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane; Transit peptide. 1.

TRANSIT 1. 57 CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 154;
                            Indels
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154 PLASTOCYANIN.
154 COPPER (BY SIMILARITY).
139 COPPER (BY SIMILARITY).
147 COPPER (BY SIMILARITY).
147 COPPER (BY SIMILARITY).
147 COPPER (BY SIMILARITY).
15577 MW; 845725D25B5F400D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rice.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                            ö
                                                                                                                                                                                                                                          PLAS ORYSA STANDARD; PRT; 154 AA. P20423; Q9SBB; 01-FBE-1991 (Rel. 17, Created) 28-FBE-2003 (Rel. 41, Last sequence update) 28-FBE-2003 (Rel. 41, Last annotation update) Plastocyanin, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 1
Pred. No. 8.1;
80.0%; Pred. No. 34; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=CV. Ilpoom; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BMBL; AF093636; AAC78108.1; -. HSSP; P00289; 2PCF.
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54.5%;
Best Local Similarity 80.0
Matches 8, Conservative
                                                                                                        127 EEVVP-GMDF 135
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1154
1154
1139
142
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58 1
139 1
142 1
147 1
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Pred. No. 8.2; Mismatches

54.5%;

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6; Conservative
Best Local Similarity
Matches 6; Conserv
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SEQUENCE
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PLAT_POPNI
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                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
STRAIN=CV. NK 1558;
MEDLINE=94039081; PubMed=8223592;
Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
 Gaps
                                                                                                                                                                                                                                                                                                                                                                  promoter region.";

Eur. J. Biochem. 217:97-104(1993).

-!- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.

-!- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURPACE IN CHLOROPLASTS.
                                                                                                                                                nordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBL_TAXID=4513;
                                                                                                                                                                                                                                            STRAIN=cv. Bomi;
Nielsen O.S., Gausing K.;
Nielsen O.S., Gausing K.;
The precursor of barley plastocyanin: sequence of cDNA clones and gene expression in different tissues.";
PEBS Lett. 225:159-162(1987).
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000923; BlueCu 1.
InterPro; IPR001235; Copper_blue.
Pfam; PR00127; copper-bind; 1.
PRINTS; PR00125; COPPERBLUE.
PRODOM; PD001215; COPPER BLUE; 1.
PROSITE; PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
 Indels
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COPPER (BY SIMILARITY).
T - N (IN CV NK 1558).
W; DAA7EABESF6F4F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 1 plastocyanin-like domain.
 3;
                                                                                                                             Last sequence update)
Last annotation update)
                                                                                              155 AA.
 Mismatches
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 5
                                                                                                                 (Rel. 08, Created)
(Rel. 08, Last seq
(Rel. 41, Last ann
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 Conservative
                                          100 EDAVPSGVDVS 110
                                                                                              STANDARD;
                      1 EEVVPXGMDYS 11
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148
120
155 AA;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transit peptide
                                                                                                                   01-AUG-1988
                                                                                                                             01-AUG-1988
28-FEB-2003
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9
                                                                                             PLAS HORVU
P08248;
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VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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METAL
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                                                                                      PLAS_HORVU
 Matches
                                                                          RESULT
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DB 1; Length 155;

Score 34;

63.0%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Malpighiales, Salicaceae, Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Distroy M.1. Egorov C.A., Donchev A.A., Atanasov B.P.;
Distroy M.1., Egorov C.A., Donchev A.A., Atanasov B.P.;
FEBS Lett. 226:17-22(1987).
-1- FUNCTION: Participates in electron transfer between P700 and the cytochrome be-f complex in photosystem I.
-1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACT IN CHIOROPLASTS.
-1- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYDAINS AND B.
-1- SIMILARITY: Contains 1 plastocyanin-like domain.
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Gape
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R HSSP; MO0199; JPLC.
R InterPro; IPR000923; Bluecu 1.
R InterPro; IPR001235; Copper_blue.
R Pam; PR00127; Copper_blue.
DR PK00127; Copper_blue; 1.
DR PK051TW; PK00156; COPPER BLUE; 1.
DR PK051TW; PK00196; COPPER BLUE; 1.
DR PK051TW; Electron transport; Copper; Thylakoid; Membrane;
EW Transit peptide; Multigene family.
FT TRANSIT 70 168 PLASTOCYANIN B.
FT CHAIN 70 168 PLASTOCYANIN B.
  ö
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=cv. Italica; TISSUB=leaf;
Reichert J., Janzelewski V., Haehnel W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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COPPER.
COPPER.
COPPER.
* P20DA6EA2038AEEA CRC64;
  ä
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
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2; Mismatches
                                                                                                                                                                                                                                                168 AA
                                                                                                                                                                                                                                                                                                                                                                                 Plastocyanin B, chloroplast precursor
                                                                                                                                                                                                                                                PRT;
  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Populus nigra (Lombardy poplar).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z50186; CAA90565.1; -. PIR; S00210; S00210. PIR; S58208; S58208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                     |: || |:| |
101 EDAVPSGVDVS 111
                                                                                                                                                                                                                                                STANDARD;
                                                      1 REVVPXGMDYS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 70-168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3691;
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01-OCT-1996 (
28-PEB-2003 (
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                                                                                                                                                                                                                                                                                   28-FBB-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Phenylalanyl-tRNA synthetase beta chain (RC 6.1.1.20) (Phenylalanine--
tRNA ligase beta chain) (PheRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98065943; PubMed=9403685;
MEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey B.K., Gwinn M.,
Dougharty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbubs J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fuji C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF03484; B5; 1.
TIGRFAMs; TIGR00471; pheT arch; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
Barbour A.G., Hinnebusch J.;
Phenylalanyl-tRNA synthetase genes (alpha and beta subunits) and thioredoxin reductase gene of Borrelia burgdorferi.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP + diphosphate + L-phenylalanyl-tRNA(Phe).

    similarity).
    SUBCELLULAR LOCATION: Cytoplasmic.
    SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN FAMILY. SUBFAMILY 2.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.0%; Score 34; DB 1; Length 566; 85.7%; Pred. No. 32; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBUNIT: Tetramer of two alpha and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;
                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAWAP, MF 00284, -; 1.
InterPro; IPR005147; B5.
InterPro; IPR004531; PheT_arch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U82978; AAB41019.1; -.
EMBL; AR001153; AAC66870.1; -.
PIR; A70164; A70164.
TIGR; BB0514; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:580-586(1997).
                                             |: || |:| |
112 BDAVPSGVDVS 122
                                                                                                                                                                                                                                            STANDARD;
1 BEVVPXGMDYS 11
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SEQUENCE 566 AA;
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Gapa

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6; Conservative

Best Local Similarity

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: Contains 3 leucine-rich (LRR) repeats.
-1- SIMILARITY: Contains 1 NB-ARC domain.
-1- DATABASE: NAME-NIB-LRRS;
NOTE-Runctional and comparative genomics of disease resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.

STRAIN-cv. Columbia;

STRAIN-cv. Columbia;

STRAIN-cv. Columbia;

SARIM M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,

Nakajima M., Iida K., Kamiya A., Narusaka M., Carninci P., Kawai J.,

Hayashizaki Y., Shinozaki K.;

Rarabidopsis thaliana full-length cDNA.",

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Potential disease resistance protein.

-I- DOWAIN: The LRR repeats probably act as specificity determinant of pathogen recognition (By similarity).

-I- SIMILARITY: Belongs to the disease resistance NB-LRR family.
                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, Rosidae,
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                  SEĞUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE-99087489; PubMed=9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat.
                                                                                                                                                     15-5RP-2003 (Rel. 42, Last sequence update)
15-5RP-2003 (Rel. 42, Last annocation update)
Probable disease resistance RPP8-like protein 4.
RPP8L4 OR AT5G48620 OR KISNI8.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRR 1.
LRR 2.
LRR 3.
ATP (POTENTIAL).
                                                                                                      908 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB015468; BAB10695.1; -.
EMBL; AKA17163; BAC4141.1; -.
INTERPO; IPR000767; Discase_resist.
INTERPO; IPR001611; I.RR.
INTERPO; IPR002182; NB-ARC.
Pfam; PP00560; I.RR; 2.
Pfam; PP00931; NB-ARC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homologs;
WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NB-ARC.
                                                                                                                                        (Rel. 42, Created)
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 5:297-308(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPP8/HRT subfamily.
|| ||||
169 VPPGMDY 175
                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
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146
575
600
                                                                                                                                    15-SEP-2003
                                                                                                    RBL4 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                             Tabata S.;
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REPEAT
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842
192
294
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                              Holub B.B., Dangl J.L.,
"Intragenic recombination and diversifying selection contribute to the evolution of downy mildew resistance at the RPP8 locus of Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                         RPPB ARATH STANDARD; PRT; 908 AA.
Q8W4J9; Q8GWG5; Q9M5A1; Q9ZSY3; Q9ZSY4;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
Disease resistance protein RPPB (Resistance to Peronospora parasitica protein 8).
                                                                                                                                                                                                                                   Arabidopsis thallana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; reptochyladons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
                                               Gaps
                                                                                                                                                                                                                                                                                                                      (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, MUTANTS RPP8-1; RPP8-2 RPP8-3, AND VARIANTS.
STRAIN-EV. Columbia, and cv. Landsberg erecta;
MEDLINE=99030193; Furbhed=9811794;
MCDDwell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEM Arabidopsis full length cDNA clones (RAFLs) sequenced
"RIKEN Arabidopsis full length CDNA clones (RAFLs) sequenced
SSP consortium (SALK/Stanford/PGEC) ";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                       Score 34; DB 1; Length 908; Pred. No. 53;
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayaahizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
104448 MW; 3111991B17239693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS
                                              2; Mismatches
                                                                                                                                                                                                                        procein 8).
RPP8 OR HRT OR AT5G43470 OR WWF20.19.
Arabidopsis thaliana (Mouse-ear crees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Di-17;
MEDLINE=20271766; PubMed=10810142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH TIP.
MEDLINE=20496823; PubMed=11041886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1). STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                             Plant Cell 10:1861-1874(1998).
                       63.0%;
            Query Match
Best Local Similarity 60...
                                                                                             883 BKLVPGGEDY 892
                                                                     1 EEVVPXGMDY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 7:31-63(2000)
 908 AA;
 SEQUENCE
                                                                                                                                           RPP8_ARATH
                                                                                                                               RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE-Functional and comparative genomics of disease resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isold=OBW4J9-2; Sequence=VSP 007171, VSP 007172;
Note=Has been shown to exist only in cv. Columbia so far;
Note=Has been shown to exist only in cv. Columbia so far;
DOMAIN: The LRR repeats probably act as specificity determinant of
pathogen recognition.
POLYMORPHISM: The strong polymorphisms present in cv. Di-17 and
cv. Columbia are probably due to an unequal crossing-over between
the highly related RPPs and RPH8A genes present in cv. Landaberg
erecta. Such variations probably modify the specificity of
                                                                                                                           the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. The interaction with TIP (TCV-interacting protein) may be essential for the recognition of the avirulence proteins, and the triggering of the
Ren T., Qu F., Morris T.J.;
"HRT gene function requires interaction between a NAC protein and viral capsid protein to confer resistance to turnip crinkle virus."; Plant Cell 12:1917-1926(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00364; DISEASERSIST.
Plant defense; ATP-binding; Repeat; Leucine-rich repeat;
Alternative splicing; Polymorphism.
DOMAIN
10 45
LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogen recognition.
MISCELLANEOUS: In cv. Columbia and cv. Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bvent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Interacts with the NAC protein TIP. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRR 1.
LRR 2.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1;
IsoId=Q8W4J9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homologs;
WWW="http://niblrrs.ucdavis.edu".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000767; Disease resist.
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF089710; AAC83165.1; -.
EMBL; AF089711; AAC7631.1; -.
EMBL; AF234174; AAF36897.1; -.
EMBL; AB025638; BAA97426.1; -.
EMBL; AY062914; AAL32992.1; -.
EMBL; AX18862; BAC43449.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     623
867
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Pfam; PF00931; NB-ARC;
                                                                                                                                                                                                                                                                                                                                                                    defense response.
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WRMLLTSRNEGVGIH -> ELLWYIHEALFLLNS (in

/FTId=VSP 007171. Missing (In isoform 2) /FTId=VSP 007172.

908

isoform 2).

|::|| | || 883 EKLVPGGEDY 892

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| Section | Sect
 (in cv. Landsberg erecta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEAK -> FLAG (in cv. Landsberg erecta). NLRVDT -> DLSVHB (in cv. Di-17). NVDTB -> SVNNK (in cv. Landsberg erecta) Q -> E (in cv. Di-17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erecta).

T -> I (in cv. Di-17).

S -> R (in cv. Di-17).

S -> R (in cv. Di-17).

H -> Q (in cv. Di-17).

I -> L (in cv. Landsberg erecta).

KNKT -> RNNA (in cv. Di-17).

K -> N (in cv. Landsberg erecta).

PRFEEDYW -> WDEDFG (in cv. Landsberg
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Y -> F (in cv. Di-17).

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C -> S (in cv. Di-17 and cv. Landsberg erecta).
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W -> C (in cv. Di-17 and cv. Landsberg erecta).
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EISTYS -> KITTQE (in cv. Di-17).

A -> V (in cv. Landsberg erecta).

E -> Q (in cv. Landsberg erecta).

DNYLSWQ -> NKYLKVH (in cv. Di-17).

DN -> NR (in cv. Landsberg erecta).
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-> H (in cv. Landsberg erecta).

-> Q (in cv. Di-17).

-> G (in cv. Di-17).
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SGK -> RGE (in cv. Di-17 and cv.
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MEDINE-99030193; PubMed-981179;

MEDINE-99030193; PubMed-9803019;

MEDINE-99030193; PubMed-980
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                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL TaxID=3702;
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Pred. No. 53;
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It defense; ATP-binding; Repeat; Leucine-rich repeat.

IN 45 LEUCINE-ZIPPER.
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                                          15-SRP-2003 (Rel. 42, Created)
15-SRP-2003 (Rel. 42, Last sequence update)
15-SRP-2003 (Rel. 42, Last annotation update)
Disease resistance protein RPH8A (RPP8 homolog A).
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Methanococcus jannaschii.
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Archaea; Buryarchaeota; Methanococci, Methanococcales;

OK NCBI TaxID=2190;

RM REHAINCABIDGOCCACCAGAE;

RM RELAINCABIDGOCCACCAGAE;

RM SEQUENCE FROW N.A.

RK STRAIN-JAL-1 / DSW 2661 / ATCC 43067;

RM SELUINS-S337999; PubMed-8880807;

RM SELUINS-S337999; PubMed-8880807;

RM SELUINS-S337999; PubMed-8880807;

RM SELUINS-S337999; PubMed-8880807;

RM KERLANGE A.R.; Dougherty B.A.; Touch J.-F., Adams M.D.; Reich C.I.;

RM KERLANGE A.R.; Dougherty B.A.; Touch J.-F., Adams M.D.; Reich C.I.;

RM KERLANGE A.R.; Dougherty B.A.; Touch J.-F.; Adams M.D.; Reich C.I.;

RM KERLANGE A.R.; Dougherty B.A.; Weinstood K.G.; Merrick J.M.; Glodek A.;

RM KERLANGE R.R.; Kirkenss B.F.; Weinstood R.G.; Merrick J.M.; Glodek A.;

RA COCTO M.D.; Roberte R.M.; Mixtel M.A.; Kaine B.P.; Mornodovsky M.;

RM Klenk H.-P.; Fraser C.M.; Smith H.O.; Woose C.R.; Venter J.C.; Geoghagen N.S.; M.; Mixtel M.O.; Woose C.R.; Venter J.C.; Geoghagen N.S.; M.; Mixtel M.O.; Woose C.R.; Venter J.C.; Gromplete genome sequence of the methanogenic archaeon, Methanococcus jamanachii.";

Science 273:1058-1073(1996).

CC This SMYSS-PROT entry is copyright. It is produced through a collaboration cromplete genome sequement is not removed. Usage by and for commercial condified and this statement is not removed. Usage by and for commercial condition and this statement is not removed. Usage by and for commercial contides requires a licenseals-sib.ch).

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RP FIR: C64417; C64417.

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BR FIR: C64417; C64417.

CG SEQUENCE 276 AA; 33454 MW; 97BBG9D392BCBFDF CRC64;

SCORES SEQUENCE 4; MISMACHER 4; MISMACHES 2; Indels 0; Gaps 0;
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Search completed: December 22, 2003, 17:42:27 Job time : 5.6 secs

1 EEVVPXGMDYS 11 | | :: | | :: | 141 EBIIENGMEHS 151

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 22, 2003, 17:27:26; Search time 25.2 Seconds (without alignments) 112.642 Million cell updates/sec Run on:

US-09-909-164-13 54 1 EEVVPXGMDYS 11 Title:

Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 segs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match O% Maximum Match 100% Listing first 45 summaries

SPTREMBL 23:\* Database

sp\_virus:
sp\_vertebrate:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\*
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sp bacteria:
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sp human:
sp invertebrate:
sp mammal:
sp mammal:
sp organele: sp plant:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Query Match Length DB ID
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SEQUENCE FROM N.A. STRAIN=FY1679; MEDLINE=94169519; PubMed=7764548;

Q9xvk4 caenorhabdi Q9a382 caulobacter Q9yii3 aeropyrum p O52680 eecherichia Q8xx15 ralstonia a		05266 escherichia 05266 escherichia 027146 methanobact 0987829 rhisobium 08thi? homo anien	Quey8 drosophila Quey8 drosophila Quey15 thermoanaer Quey19 streptococc Quey93 atreptococc Quey93 accobacill	Q8u7j0 agrobacteri Q9yet8 aeropyrum p Q29920 archaeoglob Q29451 archaeoglob	t)
Q9XVK4 6 Q9A382 7 Q9YPI3 052680 6 Q8XZL5	0 0946J7 095P46 09U6A3 017704	052673 052666 7 027146 6 098K29 08TBJ7	Q9VSY8 6 Q8RSL5 6 Q8BSL9 6 Q8DZW9	6 Q8U7JO 7 Q9YBT8 7 Q29920 7 Q29451 6 Q98FX1	a
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#### ALIGNMENTS

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STRAIN=FY1679;
MEDLINE=94019318; PubMed=8413243;
Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sherman P.; "CYC2 encodes a factor involved in mitochondrial import of yeast
                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Bukarycta; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaces.
WCBI_TaxID=4932;
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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De haan M., Maarse A.C., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      Last sequence update)
Last annotation update)
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STRAIN=HTBBB31 / DSM 14371 / JCM 11309;
STRAIN=HTBB31 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
"Molecular cloning of a gene, DHS1, which complements a drug-hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Blosci. Biotechnol. Blochem. 58:391-395 [1994].

EMBL; Z74920; CAA92201.1; -.
EMBL; Z74920; CAA69762.1; -.
SGD; S0005539; YORUIN.

SGDUSNCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
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Pred. No. 14;
                                                                                                      74.1%; Score 40; DB 3; Length 156; 77.8%; Pred. No. 2.3; tive 1; Mismatches 1; Indels
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EMBL, AP004594; BAC12465.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 319 AA; 35617 MW; 3BDAE4BF13E79B37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaeoglobus fulgidus.
Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                        (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Oceanobacillus
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                                                                                                                                                                                                                                    319 AA
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                                                                                                                  Local Similarity 77.8
les 7; Conservative
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EOLVPHGIDY 198
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Best Local Similarity
Matches 6; Conserv
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01-MAR-2003
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                                                                                                       Query Match
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Q8ESV7
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Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badgar J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Pujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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01-JAN-1998 (TERBLrel. 05, Created)
01-JAN-1998 (TERBLrel. 05, Last sequence update)
01-JAN-1998 (TERBLrel. 19, Last annotation update)
01-DEC-2001 (TERBLrel. 19, Last annotation update)
01-DEC-2001 (TERBLrel. 19, Last annotation update)
CITSPS2.
CITSPS2.
CITUS unshiu (Satsuma orange).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                          "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22255144; PubMed=12240834;
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashina K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
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Pred. No. 53;
2; Mismatches 2; Indels (
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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Pfam; PF00296; bac_luciferase; 1.
Hypothetical protein; Complete proteome.
SRQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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EMBL; AP005374; BAC09170.1; -.
                                                                                                                                                                                                                                                                               EMBL; AE001109; AAB91255.1; -. TIGR; AF2411; -.
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TLL1618.
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Best Local Similarity 63.00,
Best Local 7; Conservative
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843 EEVLPNGIGYS 853
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SEQUENCE 1044 A
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234 VIPPGMDFS 242
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Q8W568;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.
NCBI_TaxID=55188;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Sapindales; Rutaceae; Citrus.
NCBI_TaxID=55188;
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Plant Sci. 140:169-178(1999).
EMBL; AB006660; BAA22071.1; -.
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                                                                                                                              segment epidermis;
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                                                                                                                         STRAIN=cv. Miyagawa-Wase; TISSUS=Juice sacs and segment epiderr
MEDLINE=96439842; PubMed=8842155;
Komatsu A., Takanokura Y., Omura M., Akihama T.;
"Cloning and molecular analysis of CDNA encoding three sucrose
phosphate synthase isoforms from a citrus fruit (Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Komatsu A., Takanokura Y., Omura M., Akihama T.; "Cloning and molecular analysis of cDNA encoding three sucrose phosphate synthase isoforms from a citrus fruit (Citrus unshiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 36; DB 10; Length 341; 66.7%; Pred. No. 40; Live 2; Mismatches 1; Indels
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Last sequence update)
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MEDLINE-96439842; PubMed-8842155;
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Mol. Gen. Genet. 252:346-351(1996)
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Mol. Gen. Genet. 252:346-351(1996)
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228 VIPPGMDFS 236
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Cheuk R., Chen H., Kim C.J., Koesema B., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Paln C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosida II, Brassicales, Brassicaceae, Arabidopsis.
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Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Palm C.J., Quach H.L., Sarkrai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis ORP clones.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR002471; Prol_endopep_ser.
InterPro; IPR00379; Ser_estre.
BROSITE; PS00708; PRO SNDOPEP_SER; 1.
SEQUENCE 452 AA; 49682 MW; A159955B21742C4A CRC64;
                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Atig/3750/F2522 17.
Arabidopsis thallana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 50.6 kDa protein.
452 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
                                                                                                         Created)
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                                                                                                   01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bcker J.R.;
"Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 REVVPXGMDY 10
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STRAIN=CV. Columbia;
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Gaps

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6; Conservative

Matches

3 VVPXGMDYS 11

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"Structure and RPLP mapping of a rice sucrose phosphate synthase (SPS) gene that is specifically expressed in the source organ."; plant Sci. 112:207-217(1995).
                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae;
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C.,
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%; Score 36; DB 10; Length 1083; 66.7%; Pred. No. 1.5e+02; ive 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. japonica;
Sakamoto M., Satozawa T., Kishimoto N., Higo K., Shimada H.,
Fujimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001557; L_LDH.
Pfam, PP00534; Glycos_transf_1; 1.
PR051TB; PS00064; L_LDH; 1.
SEQUENCE 1084 AA; _119417 MW; 4D0D79AFEDD2P92B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122688 MW; BFC126FCA2137BB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

BU Arabidopsis sequencing project;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL049487; CAB39764.1;

EMBL; AL049487; CAB78135.1;

InterPro; IPR001295; GJVco_trans_1.

Pfam; PP00534; GJycos transfil; 1.

GJycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KU Arabidopsis sequencing project;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 13, Last sequence update)
Sucrose-phosphate synthase-like protein (EC 2.4.1.14)
P28M11.40 OR AT4G10120.
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                                                                                               PRT; 1083 AA.
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                                                                                                                                                              Created)
                                                                                                                                                           (TrEMBLrel. 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D45890; BAA08304.1;
Gramene; Q43010; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                               PRELIMINARY;
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483 VIPPGMDFS 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
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                Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler B., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,

A bunn P., Etgu P., Feldhlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A cill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A kinter J.L., Jenkins J., Johnson-Hopson C., Khan S., Knaykin B.,

A kin C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Lin S.X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A litsecher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Rad G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Suh H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Saccharum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 10; Length 460;
Pred. No. 56;
0; Mismatches 3; Indels
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EMBL, AC012679; AAG52073.1; -.

InterPro; IPR002471; Prol endopep ser.

InterPro; IPR000379; Ser estrs site.

PROSITE; PS00708; PRO_ENDOPEP_SER; 1.

Hypothetical protein.
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MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharum officinarum (Sugarcane)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%;
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Best Local Similarity 66.70,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thaliana.";
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RESULT 9
P93782
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Gaps

us-09-909-164-13.rapt

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4 VPXGMDYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=13 / Type A;
PubMed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=CFN299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XYLB1.
Rhizobium tropici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             flesh-eater.";
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                                                                                                                                                                                                                                                                                                                                                                     Putative sucrose-phosphate synthase.
P0678F11.14.
P072a sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Gill;
Weihrauch D., Towle D.W.;
Na+/H+-exchanger and Na+/K+/2Cl--cotransporter are expressed in gills of the euryhaline Chinese crab Briocheir sinensis.";
Comp. Blochem. Physiol. 126:S158-S158(2000).
EMBL; AF301160; AAG39938.1; -.
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Score 36; DB 10; Length 1084;
Pred. No. 1.5e+02;
2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 36; DB 10; Length 1100; 66.7%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Na+/K+/201-cotransporter (Fragment).
Eriocheir Sinensis (Chinese mitten crab).
Eviaryota; Metacos; Arthropoda; Crustaces; Malacostraca;
Eumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Grapsoidea; Varunidae; Eriocheir.
NTBI_TAXID=95602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gramene; Q8S064; -.
InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001557; L.LDH.
Pfam; PF00534; Glycos_transf_1; 1.
PROSITE; PS00064; L.LDH; 1.
SEQUENCE 1100 AA; 121170 MW; 084P4604BA389CAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone:P0678F11.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003437; BAB86107.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24159 MW; 599442DA26F0D3F1 CRC64;
                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                         PRT; 1100 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
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  66.7%;
66.7%;
                                               6; Conservative
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453 VIPPGMDFS 461
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469 VIPPGMDFS 477
                                                                                           3 VVPXGMDYS 11
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219 AA;
  Query Match
Best Local Similarity
Matches 6; Conserv
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SEQUENCE
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Q9GQ04;
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Submitted (DEC-1997) to the RMBL/GenBank/DDBJ databases.
-I- COFACTOR: ZINC (BY SIMILARITY)
-I- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                         Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium.
Score 35, DB 5, Length 219;
Pred. No. 39;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein; Complete proteome.
253 AA; 27714 MW; 814DF79D3E0D7486 CRC64;
                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
EPEO057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aryl-alcohol dehydrogenase homolog (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002). RMBL; AP003185; BAB79763.1; -. InterPro; IPR000205; NAD binding. InterPro; IPR000594; ThiF_domain. Pfam; Pro) 1970999; ThiF; 1. Hypothetical protein; Complete proteome. SRQUENCE 253 AA; 27714 MW; 8140F79D3E0D7486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 A.A.
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InterPro; IPR002328; ADH zinc.
InterPro; IPR002085; Adh zin Emily.
InterPro; IPR0002085; NAD_binding.
  Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                               PRELIMINARY;
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108 BEIIPDDVDY 117
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DR Pfam; PF00107; adh_zinc; 1.

DR PROSITE; PS00059; ADH_ZINC; 1.

KW Metal-binding; Oxidoreductase; Zinc; Plasmid.

FT NON TER 298 AP; 31092 MW; 49B2F8117C33AB87 CRC64;

Query Match 64.8%; Score 35; DB 2; Length 298;

Best Local Similarity 50.0%; Pred. No. 55;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EVVPXGMDYS 11

|::| | | | | | | |

Db 250 EIIPEGADFS 259

Search Completed: December 22, 2003, 17:51:30

Job time: 26.2667 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 22, 2003, 16:41:00 ; Search time 32.4667 Seconds (without alignments) 53.778 Million cell updates/sec Run on:

US-09-909-164-42 52 1 BEVVHXQXHYS(11) Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 seqs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*
| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1983.DAT:\*
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| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1986.DAT:\*
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Hepatitis C virus	Hepatitis C virus	Hepatitis C virus	Hepatitis C virus	U	Hepatitis C virus	Ü	Hepatitis C virus	Hepatitis C virus
SUMMARIES	ΩI	ABB80546	ABB80550	ABB80554	ABB80555	ABB80523	ABB80527	ABB80531	ABB80532	ABB80537
	80	23	33	23	53	23	23	23	23	23
	Query re Match Length DB II	11	11	11	11	11	11	#	11	11
•	Query Match	94.2	94.2	94.2	94.2	92.3	92.3	92.3	92.3	92.3
	Score	49	49	49	49	48	48	48	48	48
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48 92.3 48 92.3 49 92.3	0 76	76.	76.	76.	76.	75						7.5		75	9 75.	9 75.	75.	75.	75.	75.	75.	75.	75.	75.		
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ALIGNMENTS

ABB80546 standard; peptide; 11 AA. ABB80546;

(first entry) 08-OCT-2002

Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide. Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #26. RESULT 1

ABB8 0546

ID ABB8

XX ABB8

XX ABB8

XX YIT

XX XIT

Synthetic.

/note= "N-terminal acetyl" Location/Qualifiers Key Modified-site

/note= "Norvalyl carbonyl forming keto-amide linkage with residue ?" Modified-site

11 /note= "C-terminal amide" Modified-site

WO200208251-A2

31-JAN-2002.

19-JUL-2001; 2001WO-US23169.

21-JUL-2000; 2000US-220101P.

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/note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
                                                                                                                                                   The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmacceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                          otide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #30
                                                                                                                                                                                                                                                                                   Score 49; DB 23; Length 11; Pred. No. 0.0037;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "N-terminal acetyl"
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                         Brunck TK;
                                                                                                                             Claim 17; Page 65; 69pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB80550 standard; peptide; 11
                                                                                                                                                                                                                                                                                   94.2%;
90.9%;
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(CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                       1 EEVVPXGXHYS
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                                                  MPI; 2002-361643/39
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                            11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                     virus protease
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                                                                             Novel peptide
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                         Lim-wilby M,
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                                               The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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residue 7"
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                                                                                                                                                                                          Score 49; DB 23; Length 11; Pred. No. 0.0037;
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                           Claim 17; Page 65; 69pp; English
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90.9%;
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Best Local Similarity
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    residue 7"
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                                                           Score 49; DB 23; Length 11;
Pred. No. 0.0037;
0; Mismatches 1; Indels
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10s 10; Conservative
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  Score 49; DB 23; Length 11
Pred. No. 0.0037;
0; Mismatches 1; Indels
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Pred. No. 0.0058;
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Query Match
Best Local Similarity 90.9
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                             Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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virucide.
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               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11
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Pred. No. 0.0058;
0; Mismatches 1; Indels
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                                              ABB80527 standard; peptide; 11 AA
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90.9%;
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21-JUL-2000; 2000US-220101P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
             /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                             peptide compound having hepatitis C virus protease inhibitory ity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17.
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                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 23; Length 11;
Pred. No. 0.0058;
0; Mismatches 1; Indels
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/note= "N-terminal acetyl"
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                                              /note= "D-form residue"
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                                                                                                                                                                           Brunck TK;
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                                                                                                                                                                                                                                                  Claim 17; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                              92.3%;
90.9%;
                                                                                                                     19-JUL-2001; 2001WO-US23169
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                                                                                                                                                        (CORV-) CORVAS INT INC
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les 10; Conserv
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                   Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.3%; Score 48; DB 23; Length 11; 90.9%; Pred. No. 0.0058; 1ive 0; Mismatches 1; Indels
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                                                                                                                                                                                         Brunck TK;
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19-JUL-2001; 2001WO-US23169.
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activity useful for treating disorders associated with hepatitis
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                                                                                                                    The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38.
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                                                                                                                                                                                                                  DB 23; Length 11; 0.0058; Indels
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Pred. No. 0.005
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                             Brunck TK;
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                                                                                                     Claim 17; Page 65; 69pp; English
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Best Local Similarity 90.9%;
Matches 10; Conservative (
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                             Lim-wilby M, Levy OE,
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          (CORV-) CORVAS INT INC
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                                               WPI; 2002-361643/39.
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                                                                                    virus protease
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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Pred. No. 0.0058;
0; Mismatches 1; Indels
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Claim 17; Page 65; 69pp; English
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Local Similarity 90.9%;
hes 10; Conservative
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Gaps

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Length 11;

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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) procease inhibitory activity. The peptides of the invention are alpha ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protesse. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #24
                                                                                                                                                                  Score 48; DB 23;
Pred. No. 0.0058;
                                                                                                                                                                                                Mismatches
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90.9%;
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                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                    11 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a peptide compound of the invention having hepatitis C virus (HVV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                   Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ptide compound having hepatitis C virus protease inhibitory useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #25.
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 DB 23; Length 11;
0.23;
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                        2; Indels
                       Mismatches
                                                                                                                                                                                                                                                                                                                        'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                             /note= "C-terminal amide"
  Score 40;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                      'note= "D-form residue"
                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                    ABB80545 standard; peptide; 11 AA.
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76.9%;
ilarity 81.8%;
Conservative
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                                                                                                                                                                                    (first entry)
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                                                1 EEVVPXGXHYS 11
                                                                      REVVPXGTSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levy OE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-361643/39.
            Similarity
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                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus protease
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                         6
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Query Match
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                  /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
                                                                                                                 Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide,
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide compound having hepatitis C virus protease inhibitory sectivity useful for treating disorders associated with hepatitis C virus protease -
                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 23; Length 11;
Pred. No. 0.23;
0; Mismatches 2; Indels
                                                                                                                                                                                                                       'note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
                                                                                                                                                                                         Location/Qualifiers
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ABB80547 standard; peptide; 11 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 81.8%;
9; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-2000; 2000US-220101P
                                                        08-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-361643/39.
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Best Local Similarity
Matches 9; Conserv
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Modified-site
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                           ABB80547;
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Search completed: December 22, 2003, 17:41:02 Job time : 33.4667 sec8 1 EEVVPXGTDYS 11 g

1 BEVVPXGXHYS 11

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Sequence 21444, A Sequence 4794, Ap Sequence 3, Appli Sequence 1711, Ap Sequence 182, Appl Sequence 182, Appl Sequence 2, Appli Sequence 66, Appli Sequence 66, Appli Sequence 66, Appli Sequence 66, Appli Sequence 10, Appli
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Sequence 3, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 9, Appli
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                                                                                                     December 22, 2003, 16:37:03 ; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
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.: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-134-001C-4794
US-09-134-001C-4794
US-08-134-001C-4794
US-08-134-001C-4794
US-08-134-001C-4794
US-08-15-096-3
US-09-107-532A-6771
US-08-961-083-182
US-08-821-119-19
US-08-821-119-19
US-08-821-119-2
US-08-961-083-66
US-08-961-083-66
US-08-961-083-66
US-09-536-784-66
US-09-530-010-7
US-08-530-010-7
US-08-530-010-7
US-08-530-010-1
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US-08-484-101B-7
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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52
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Match Length DB
                                                                                                                                                                                      Title:
Perfect score:
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No.
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8 61.5 738 2 US-08-484-101B-9 Sequence 9, Appli 561.5 738 2 US-08-484-101B-11 Sequence 11, Appl	!	24D-3 Sequence 3, Appli	24D-5 Sequence 5, Appli				_		Sequence 4185, Ap	Sequence 7284, Ap	Sequence 15, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 28, Appl	Sequence 2, Appli
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	08-SD	US-08-714-52	US-08-714-52	US-08-714-524D-7	US-08-714-524D-	US-08-714-524D-11	US-09-252-991A-32960	US-09-134-001C-3950	US-09-134-001C-4185	US-09-328-352-7284	US-08-178-257-15	US-09-342-647-4	US-08-459-146-2	US-08-459-065-2	US-09-342-647-2	US-09-342-647-28	US-09-621-816B-2
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61.5	738	738	738	738	738	738	1247	70	237	252	388	505	622	622	630	667	700
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# ALIGNMENTS

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Sequence 21444, Application US/09252991A
Petent No. 6551795
PETENTAL INFORMATION: AEROIGAGE ALTO AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
PILLA SEPERANCE: 10.1736.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: 1999-02-18
PRIOR APPLICATION NUMBER: 1999-02-18
PRIOR APPLICATION NUMBER: 1999-02-18
PRIOR APPLICATION NUMBER: 1999-07-7
PRIOR PILLING DATE: 1999-07-7
PRIOR PLING DATE: 1999-07-7
PRIOR PLING APPLICATION NUMBER: 1999-07-7
PRIOR APPLICATION NUMBER: 1999-07-7
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; Patent No. 6008194
; GENERAL INFORMATION:
APPLICANT: Lal. Preeti
; APPLICANT: Lal. Preeti
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; CORRESPONDENCES: 4
; CORRESPONDENCE ADDRESS: 3
; ADDRESSER: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPTWARE: PSESSOG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,096
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/879,995
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billing, Lucy J. 79
REGISTRATION NUMBER: 36,749
TRIERCOMMUNICATION INFORMATION:
TRIERCHONE: 415-855-0555
TELEFRAX: 415-845-4166
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0326 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFRAX: 415-845-4166
                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 66.7
Matches 6; Conservative
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 163590
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CLONE: 163590
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ## Sequence 26615, Application US/09252991A
## Sequence 26615, Application US/09252991A
## Sequence 26615, Application US/09252991A
## Petent No. 6551795
## GENERAL INFORMATION:
## TITLE OF INVENTION:
## APPLICATION NUMBER:
## US/09/252,991A
## CURRENT FILING DATE: 1999-02-18
## PRIOR FILING DATE: 1999-02-18
## PRIOR FILING DATE: 1998-02-18
## PRIOR FILING DATE: 1998-07-27
## NUMBER OF SEQ ID NOS: 33142
## UNMER OF SEQ ID NOS: 33142
## UNMER OF SEGIS
## US/09/2019 ## UND 26615
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                                                                                                Query Match
Best Local Similarity 63.6%; Pred. No. 47;
Matches 7; Conservative 1; Mismatches 3; Indels
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Patent No. 5985606
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STRET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COMPUTRY: USA
COMPUTRY: USA
COMPUTRY: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
HILL OF DATE: HARDABLE FORM:
MEDLICATION DATA:
HILL OF DATE: HARDABLE FORM:
MEDLICATION DATA:
HILL OF DATE: HARDABLE FORM:
HEADLICATION DATA:
HEADLICATION DATA:
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HEADLICATION DATA:
HARDADATENT HARDAMITH DATE:
HARDAMIT
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      ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4794
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 63.6
Matches 7; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: Herewith
                                                                                                                                                                                                                                                                               1 EEVVPXGXHYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-26615
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Sequence 182, Application US/08961083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS PAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
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                                                                        65.4%; Score 34; DB 3; Length 126; 66.7%; Pred. No. 12;
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                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USAL

ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPR: CD/ROM ISO9660
COMPUTER: PC
COMP
                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...63
SEQUENCE DESCRIPTION: SEQ ID NO: 6771:
US-09-107-532A-6771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6771, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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BRIMAFGDHYN 15
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                                                                                                                                                                                                                                                              28 EQVVPGGGH 36
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US-09-215-096-3
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RESULT 7 US-08-961-083-182

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Sequence 182. Application US/09536784

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences, Inc.
GITY: Rockville
CITY: Rockville
STATE: Maryland
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
PARENT NO. 6159469
GENERAL INPORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 3; Length 447; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII TAXL CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/536,784 FILING DATE: 30-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM:
SOFTWARE: AGCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
FRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BICOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: 98346
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8514
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-961-083-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| | ||
178 IVPHGGHY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VVPXGXHY 10
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## STRANDEDNESS: single
### MOLECULA TYPE: protein
### MOLECULA TYPE: protein
### SEQUENCE DESCRIPTION: SEQ ID NO: 56:

US-09-536-784-56

Query Match
Best Local Similarity 62.5%; Pred. No. 1.4e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0

Qy 3 VVPXGXHY 10

| | | | | | |

Db 185 IVPHGDHY 192

Search completed: December 22, 2003, 16:43:44

Job time: 10.1333 secs
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(without alignments)
98.451 Million cell updates/sec
                                                                                                                                                                                            December 22, 2003, 16:40:14 ; Search time 20.8667 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    696363 seqs, 186758610 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                  US-09-909-164-42
52
1 EEVVPXGXHYS 11
                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Appl	Appl	Appl	Appl	Appl	Appl	App	Appl	Appl	Appl	App1	App.	Appli	Appli	Appl
_	24,	16,	16,	15,	15,	18,	82,	38,	24,	9	9	194	. 6	7.	10,
Description	Seguence 24,	Sequence 16,	Sequence 16,	Sequence	Sequence 15,	Sequence 18,	Sequence 182,	Sequence	Sequence 24,	Sequence 6	Sequence 5	Sequence	Sequence 8, Appli	Sequence 7, Appl	Sequence 10,
ΩΙ	US-09-769-736-24	US-09-252-088-16	US-10-340-792-16	US-09-252-088-15	US-10-340-792-15	US-09-769-736-18	JS-09-765-272-182	US-09-769-787-38	US-09-769-744A-24	JS-09-765-272-66	JS-09-765-272-56	US-09-769-787-194	US-09-884-465A-8	US-09-884-465A-7	US-09-884-465A-10
038	•	11	12	11	12	12	6	11	12	6	0	11	11	1	11
Query Match Length DB	381	715	715	793	793	822	447	484	484	763	796	826	838	840	840
Query Match	65.4	65.4	65.4	65.4	65.4	65.4	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5
Score	34	34	34	34	34	34	33	33	33	33	33	33	33	33	33
Result No.		7	e	4	ស	Q	7	œ	6	10	11	12	13	14	15
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Sequence 6, Appli	Sequence 32486, A		Sequence 24, Appl	Sequence 11332, A	16	36	Sequence 38, Appl	36	22	34		1321	Sequence 104, App	Sequence 31, Appl	Sequence 8, Appli	0416	Sequence 27, Appl	, 10,	Sequence 4919, Ap	Sequence 26, Appl	'n	6		7	4	č	č	9	Sequence 2, Appli
							US-10-171-404A-38	US-10-171-404A-36	US-10-176-847-22	US-10-205-823-343	US-09-881-752A-292	US-10-156-761-13210	US-10-279-029-104	US-10-219-810-31	US-10-177-293-8	US-09-815-242-10416	US-10-298-638-27	US-10-298-638-10	US-09-738-626-4919	US-09-820-843A-26	US-09-942-447-2	US-10-391-399-61	US-10-319-762-2	US-10-032-585-7521	US-10-122-067-4	US-10-262-794A-32	US-10-242-056-32	US-10-096-534-67	US-10-122-067-2
11	12	12	12	15	11	12	12	12	15	15	10	15	12	12	15	σ	12	12	10	Ξ	10	12	15	12	12	12	15	12	12
1039	153	345	345	499	519	519	717	738	1463	1463	44	217	354	354	364	387	482	485	622	653	999	999	700	761	1163	1485	1485	1499	1499
63.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	59.6	9.69	9.69	59.6	9.65	9.69	9.69	9.69	9.69	9.69	59.6	59.6	59.6	9.69	59.6	9.69	9.69	9.69	9.69
33	35	32	32									31							31	31	31	31	31	31	31	31	31	31	31
16	17	18	19	20	71	55	23	24	25	56	27	58	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

RESULT 1
US-09-769-736-24
US-09-769-736-24
SEQUENCE 24, Application US/09769736
Publication No. US20030138775A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Mells, Jeremy M
APPLICANT: Wells, Jeremy M
APPLICANT: Wells, Sean B
ITILE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21089wo
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PATENT NOS: 212
SOFTWARE: PATENT NOS: 212
SOFTWARE: PATENT NOS: 21

ALIGNMENTS

TYPE: PRT

ORGANISM: Streptococcus agalactiae

US-09-769-736-24

Query Match

Best Local Similarity 75.0%; Pred. No. 98;

Matches 6; Conservative 0; Mismatches 2; Indels

Qy 3 VVPXGXHY 10 ||| || || Db 350 VVPHGDHY 357

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Gaps

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RESULT 2 US-09-252-088-16 ; Sequence 16, Application US/09252088 ; Publication No. US20030031682A1

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Gaps
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US-10-340-792-15

i Sequence 15, Application US/10340792

i Sequence 15, Application US/10340792

i Publication No. US20030228323A1

i GENERAL INFORMATION:

APPLICANT: BOYER, Martine

APPLICANT: CHARLEBOIS, Isabelle

APPLICANT: HAMEL, Josee

APPLICANT: MARTIN, Denis

TITLE OP INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS

FILE REFRERENCE: 8331-9002

CURRENT APPLICATION NUMBER: US/10/340,792

CURRENT FILING DATE: 2003-01-13

FRIOR APPLICATION NUMBER: US/60/252,088B

FRIOR FILING DATE: 1999-02-18

FRIOR PILING DATE: 1999-02-18

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PARENTIN Ver: 2.0

SEQ ID NO 15

LENGTH: DATE: DATE

TWOR: DATE: DATE

THENDER OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 65.4%; Score 34; DB 12; Length 793; Best Local Similarity 75.0%; Pred. No. 2.1e+02; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.4%; Score 34; DB 11; Length 793; 75.0%; Pred. No. 2.1e+02;
                                         APPLICANT: LARALLIA. JOSE
APPLICANT: HAMEIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
TILE REPERRACE: 8331-9002.
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US/60/075,425
RANLIER APPLICATION NUMBER: US/60/075,425
NUMBER OF SEQ ID NOS: 44
SEQ ID NOS: 42
SEQ ID NOS: 42
SEQ ID NOS: 42
SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-769-736-18
; Sequence 18, Application US/09769736
; Publication No. US20030138775A1
; GENERAL INFORMATION:
; APPLICANT: Merobial Technics Limited
; APPLICANT: Wells, Jeremy M
; APPLICANT: Wells, Jeremy M
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins

    TYPE: PRT
    ORGANISM: group B streptococcus
US-10-340-792-15

                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT CORGANISM: group B streptococcus US-09-252-088-15
APPLICANT: BOYER, Martine APPLICANT: CHARLEBOIS, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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Pred. No. 1.9e+02;
0; Mismatches 2; Indels
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US-10-340-792-16

Sequence 16, Application US/10340792

Publication No. US2003022833A1

GENERAL INFORMATION:
APPLICANT: BRODGUR, Bernard R.
APPLICANT: BOYER, Martine
APPLICANT: BOYER, Martine
APPLICANT: HAWEL, Josee
APPLICANT: HAWEL, Josee
APPLICANT: HAWEL, Josee
APPLICANT: MARTIN, Denis
ITILE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 8331-9002
CURRENT FILING DATE: 2003-01-13
FRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

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PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18
                        APPLICANT: BRODEUR, Bernard R.
APPLICANT: BRODEUR, Bernard R.
APPLICANT: BOYER, Martine
APPLICANT: CHARLEBOIS, Isabelle
APPLICANT: CHARLEBOIS, Isabelle
APPLICANT: CHARLEBOIS, Isabelle
APPLICANT: MARTIN, Donis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 8331-9002
CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT APPLICATION NUMBER: US/60/075,425
EARLIER FILING DATE: 1999-02-18
SARLIER FILING DATE: 1999-02-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/09252088; Publication No. US20030031682A1; GENERAL INFORMATION:
APPLICANT: BRODEUR, Bernard R.
APPLICANT: RIOUX, Clment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: group B streptococcus
US-09-252-088-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.4%;
Best Local Similarity 75.0%;
Matches 6; Conservative (
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Best Local Similarity 75.0
Matches 6; Conservative
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   GENERAL INFORMATION:
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LENGTH: 715
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SEQ ID NO 24
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Patent No. US20020061545A1

GENERAL INFORMATION:

APPLICANT: Choi et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

NUMBER OF SEQUENCES: 452

CORRESPONDENCE ADDRESS:

ADDRESSE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ACSTI TEAK
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIPICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/961,083
FILING DATE: *CUNKNOWN»
APPLICATION NUMBER: 08/961,083
FILING DATE: *CUNKNOWN»
ATTORISY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REFERENCE/DOCKET NUMBER: 98340P2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                              Score 34; DB 12; Length 822;
Pred. No. 2.2e+02;
0; Mismatches 2; Indel8
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FILE REFERENCE: PWC/P21089wo
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT FILING DATE: 2003-02-14
FRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PAECHEIN Ver. 2.1
SOFTWARE: 922
LENGTH: 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 182:
US-09-765-272-182
                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-09-769-736-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (301) 309-8512
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication US/09769744A

| Publication No. US20030134407A1
| GENERAL INFORMATION:
| APPLICANT: Le Page, Richard WF
| APPLICANT: Handiffy, Sean B
| TITLE OF INVENTION: Proteins |
| FILE REPERRIES: PWC/P21122MO
| CURRENT APPLICATION NUMBER: US/09/769,744A
| CURRENT FILING DATE: 1999-07-27
| PRIOR FILING DATE: 1999-07-27
| PRIOR PILING DATE: 1999-07-27
| PRIOR PILING DATE: 1999-07-27
| PRIOR PILING DATE: 1999-07-27
| PRIOR FILING DATE: 1999-03-19
| NUMBER: OF SEQ ID NOS: 1969-03-19
                                                                 APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129W0
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT APPLICATION NUMBER: GB 9816337.1
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver. 2.1
SENGTH: 484
; Sequence 38, Application US/09769787; Publication No. US20030091577A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus pneumoniae US-09-769-787-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptococcus pneumoniae US-09-769-744A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : PatentIn Ver. 2.1
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Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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202 IVPHGGHY 209
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Pred. No. 3.5e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.5%; Score 33; DB 9; Length 796; 62.5%; Pred. No. 3.4e+02; ive 1; Mismatches 2; Indels
                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/961,083
FILING DATE: cunknown:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 96,373
REFERENCE/DOCKET NUMBER: PB340P2
TELESPAN: (301) 309-8512
INPORMATION FOR SEQ ID NO: 56:
BEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 194, Application US/09769787
; Bequence 194, Application US/09769787
; Publication No. US20030091577A1
; GENERAL INPORMATION:
; APPLICANT: Midrobial Technics Limited
; APPLICANT: Glibert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-19
; REIOR PRILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 194
                     APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-194
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                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%;
62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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185 IVPHGDHY 192
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Sequence 56, Application US/09765272

Ratent No. US20020061545A1

GENERAL INFORMATION:

APPLICANT: Choi et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452

CORRESPONDENCE: 452

CORRESPONDENCE: HUman Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA
                                                                                                                  APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
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                                                                                                                                                                                                                                                                                                                                                                     CURDITES AND CONTOUR TYPES DISABLE AS 150 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
COPERATING SYSTEM: MSDOS version 6.2
SOFTWARS: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 2-Jan-2001
CLASSIFICATION: -UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: -UNKnown>
ATTONNEY/AGRT INFORMATION:
NAME: BIOCOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET WUNBER: P8340P2
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.5%; Score 33; DB 9; Length 763; Best Local Similarity 62.5%; Pred. No. 3.2e+02; Matches 5; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-765-272-66
                                              Sequence 66, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                  STATE: Maryland COUNTRY: USA
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Gaps

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Score 33; DB 11; Length 840; Pred. No. 3.6e+02; 1; Mismatches 2; Indels

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CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin version 3.1
LENGTH: 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 22, 2003, 17:32:44
Job time : 21.9333 secs
                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                               Query Match 63.5%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                     055190-0044
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182 IVPHGGHY 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 11; Length 838;
Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
## APPLICANT: Brodeur, Bernard
## APPLICANT: Martin, Denis
## APPLICANT: Charland, Nathalie
## APPLICANT: Charland, Nathalie
## APPLICANT: Charland, Nathalie
## APPLICANT: Charland, Nathalie
## TITLE OF INVENTION: Streptococcus
## CURRENT APPLICATION NUMBER: US/09/884,465A
## CURRENT FILING DATE: 2000-06-20
## PRIOR APPLICATION NUMBER: 60/212,683
## PRIOR PILING DATE: 2000-06-20
## NUMBER OF SEQ ID NOS: 384
## SOFTWARE: PatentIn version 3.1
## SCOTTWARE: PatentIn version 3.1
## SCOTTWARE: Streptococcus pneumoniae
## ORGANISM: Streptococcus pneumoniae
## US-09-884-465A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7. Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Marchin, Denis
APPLICANT: Marthin, Denis
APPLICANT: Charland, Nathalie
FILE REFERENCE: 055190-0044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denia
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/884,465A CURRENT FILING DATE: 2001-06-20 PRIOR APPLICATION NUMBER: 60/212,683 PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09884465A Publication No. US20030077293A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 840
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Best Local Similarity 62.5
Matches 5; Conservative
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us-09-909-164-42.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 22, 2003, 17:24:36; Search time 9.0667 Seconds (without alignments) 116.675 Million cell updates/sec Run on:

US-09-909-164-42 52 Title:

1 EEVVPXGXHYS 11 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: \* 2: pir2: \* 3: pir2: \* 4: pir4: \* PIR 76:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	DNA binding protei	protei		lependent	L-shaped tail fibe	V1 protein - tobac	tachykinin B precu		hypothetical prote		hypothetical 92.4K	carbamoy1-phosphat	hypothetical prote	trans-regulatory s	conserved hypothet	hypothetical prote	2-methyl-branched-	hypothetical prote	TSI8.1 protein - A	hypothetical prote	conserved domain p	conserved domain p	hypothetical prote	conserved hypothet	hypothetical prote	histidine Motif-Co	conserved hypothet	hypothetical prote	probable monoxygen
SUMMARIES	ID	T02590	A72207	E69086	AF3286	S36851	A42452	A25905	C75538	T28717	A69284	T46758	F89892	E97985	VKLJSI	D82618	AE2001	A48702	869046	G86430	538143	C95136	B95136	E98004	G95115	C97985	D98004	H95115	D97985	A70939
	DB	7	~	~	~	~		~							н	N	~	~	~	N	~	N	~	N	N	7	~	~	N	N
	Query Match Length	233	308	360	1028	1396	102	126	279	495	534	822	1057	46	124	156	252	412	460	510	743	802	819	828	839	853	855	1039	1039	162
	Query Match	67.3	67.3	67.3	67.3	67.3	65.4	65.4	65.4	65.4	65.4	65.4	65.4	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	61.5
	Score	35	35	35	. 32	35	34	34				34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	32
	Result No.	-	7	3	4	'n	9	7	Φ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

hypothetical prote	prohibitin 2 [impo	GMP synthetase, su	hypothetical prote	fructose-bisphosph	hypothetical prote	probable aspartate	hypothetical prote	probable non-photo	probable bZIP tran	aldehyde dehydroge	DNA mismatch repai	phage transposase	hypothetical prote	macrophage-stimula	ethylene-response
857810	CSPIPA	H69194	AF3211	847540	T17267	G69119	T24111	G96568	G84598	AI3544	A69663	A91247	\$61239	JC5061	A48246
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225	786	311	322	364	369	374	425	454	519	536	627	969	701	716	738
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61.	7	61	61	61	61	61	61	61	61	61	61	61	61	61	61
32	75	32	35	32	32	32	32	32	32	32	32	32	32	32	32

## ALIGNMENTS

-	
RESULT	T02590

DNA binding protein EREBP-2 - common tobacco CiSpecies: Nicotiana tabacum (common tobacco) CiSpecies: Tobaccos; TOS590 Richard, M.; Shinshi, H. Plant Cell 7, 173-182, 1995 Richard Cell 7, 173-182, 1995 Aylities: Ethylene-inducible DNA binding proteins that interact with an ethylene respon A;Reference number: Z14671; MUID:95276459; PMID:7756828 A;Accession: T02590 A;Accession: T02

Gaps ö h Similarity 60.0%; Pred. No. 9.8; Similarity 60.0%; Pred. No. 9.8; 6; Conservative 1; Mismatches 3; Indele Best Local Similarity Matches 6; Conserv Query Match

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1 BEVVPXGXHY 10

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90 QAVVPKGRHY 99

fish proteinase activity modulator HflK - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: In-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000
C;Accession: A72207
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hick.
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D

Nature 399, 323-329, 1999
A.Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome 8. A.Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome 8. A.Reference number: A72207
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: DNA
A.Residues: 1-308 <ARN>
A.Status: DNA
A.Status: DNA
A.Status: DNA
A.Gross-references: GB:AE001819; GB:AE000512; NID:g4982396; PIDN:AAD36885.1; PID:g4982-G-Genetics:
A.Gene: TM1822
C.Superfamily: erythrocyte band 7 integral membrane protein

Gaps ö Query Match 67.3%; Score 35; DB 2; Length 308; Best Local Similarity 75.0%; Pred. No. 13; Matches 6; Conservative 0; Mismatches 2; Indels

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A; Molecule type: DNA
A; Readdues: 1-1396 «KAL»
A; Readdues: 1-1396 «KAL»
A; Crose-references: EMBL:
A; Crose-references: EMBL:
A; Crose-references: EMBL:
B; Kaliman, A.V.; Kryukov, V.M.; Bayev, A.A.
Nucleic Acids Res. 16, 6230, 1988
A; Title: The nucleotide sequence of bacteriophage T5 DNA at the region between early a:
A; Title: The nucleotide sequence of pacteriophage T5 DNA at the region between early a:
A; Reference number: S01982; MUID: 88289370; PMID: 3267228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VI protein - tobacco yellow dwarf virus (strain Australia)
C;Species: tobacco yellow dwarf virus
C;Species: tobacco yellow dwarf virus
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C;Accession: A42452
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
R;Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
A;Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yel
A;Reference number: A42452; MUID:92188538; PMID:1546458
R;Kaliman, A.V.; Kulshin, V.E.; Shlyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NiAlterrate names: neuromedin K
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: A25905
R;Koteni, H.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 7074-7078, 1986
A;Title: Structure and gene organization of bovine neuromedin K precursor.
A;Reference number: A25905; MUID:86313713; PMID:3462746
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A;Realdues: 1-126 <KOT>
A;Cross-references: GB:N41351; NID:g163587; PIDN:AAA30723.1; PID:g163590
C;Superfamily: neurokinin B precursor
P;1-26/Domain: signal sequence #status predicted <SIG>
P;27-126/Product: protachykinin B #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284
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                     FBBS Lett. 366, 46-48, 1995
A/Title: The nucleotide sequence of the bacteriophage T5 ltf gene.
A/Reference number: 865934; MUID:95309401; PMID:7789514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 35;
Local Similarity 50.0%; Pred. No. 6
les 5; Conservative 2; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Keywords: late protein; tail fiber
                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 934-985,'A',987-1396
A,Crose-references: EMBL:X07559
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                    A; Accession: 801984
A; Status: translation not shown
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A, Molecule type: DNA
A, Residues: 1-102 <MOR>
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                                                                                                                                                                                C. Species: Methanobacterium thermoautotrophicum (strain Delta H)
C. Species: Methanobacterium thermoautotrophicum
C. Species: Methanobacterium thermoautotrophicum
C. Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C. Accession: B69086
R. Shaith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wieczbowski, J.; Gibson, R.; Jiwani, N. Xi, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A. Aritle: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A. Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reaiduea: 1-360 <MTH>
A;Crosa-referencea: GB:AE000923; GB:AE000666; NID:g2622766; PIDN:AAB86115.1; PID:g262277
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, B.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-dependent DNA helicase BME10275 [imported] - Brucella melitensis (strain 16M)
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A,Molecule type: DNA
A,Residues: 1-1028 «XUR»
A,Cross-references: GB:AB008917; PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190
A,Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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N'Alternate names: ltf protein
C;Species: phage TS
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 17-Nov-2000
C;Accession: S65934; S01984; $38851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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Pred. No. 49;
2; Mismatches
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Pred. No. 16;
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Best Local Similarity 54.5
Matches 6; Conservative
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98 EDLVPMGSHHT 108
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76 BKIVPPGARYS
WPXGXHY 10
                                                 41 WPSGIHY 48
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Best Local Similarity
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Coenzyme F420-quinone oxidoreductase (EC 1.6.5.-) 56K chain - Archaeoglobus fulgidus CiSpecies Archaeoglobus fulgidus C;Species Archaeoglobus fulgidus C;Species Archaeoglobus fulgidus C;Species Archaeoglobus fulgidus C;Species Archaeoglobus fulgidus C;Date: 05-Dac-1997 #sequence_revision 05-Dec-1997 #text_change 19-may-2000 C;Accession, A69284; 345665.

C;Accession, A69284; 345665.

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dode S;Klenk, A.D.; A. Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 190, 164-770, 1997 **Authors Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; McDonald, L. A;Authors Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; McDonald, L. A;Authors Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woses, C.R.; Venter, J.C.

A;Authors Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woses, C.R.; Venter, J.C.

A;Authors Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smither The complete genome sequence of the hyperthermophilic, sulfate-reducing archs A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Reference number: A69250; MUID:98133340; Translation not shown
A;Molecule type: DNA
A;Reference number: B45665; MUID:94333340; PMID:8055920
A;Attle: F(420)H(2): quinone oxidoreductase from Archaeoglobus fulgidus. Characterizat A;Reference number: S45665; MUID:94333340; PMID:8055920
A;Residues: Z;X:4,X:6-7,X:9-10,XX:13-14 <KUN>
A;Notecule type: Drotein
A;Residues: Z;X:4,X:6-7,X:9-10,XX:13-14 <KUN>
A;Notecule type: Drotein
A;Residues: Z;X:4,X:6-7,X:9-10,XX:13-14 <KUN>
A;Notecule type: Drotein
A;Residues: Could not distinguish between glutamate and cysteine for residues C;Superfamily: glutamate synthase small chain
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Cipate: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
Cipate: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
Cipate: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
Rispellarberg, B.; Rozdzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzler, N.; Lu
Infect. Immun. 67, 871-878, 1999
A.Title: Lmb, a protein with similarities to the Lral adhesin family, mediates attachm
A.Title: Lmb, a protein with similarities to the Lral adhesin family, mediates attachm
A.Atterence number: Z24091; MUID:99115568; PMID:9916102
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: DNA
A.Residues: 1-822 <SPE>
A.Residues: 1-822 <SPE>
A.Residues: BMBL:AF062533; NID:94249622; PIDN:AAD13797.1; PID:94249624
A.SEperimental source: strain R268
Cisuperfamily: Streptococcus agalactiae hypothetical 92.4K protein
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45.5%; Pred. No. 39;
tive 3; Mismatches 3; Indels
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Best Local Similarity
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wes 6; Conserv
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Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cispecies: Deinococcus radiodurans
Cispecies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
Ciscoccus radiodurans
Ciscoccus radiodurans
R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75538
A;Accession: C75538
A;Retsidues: preliminary
A;Retsidues: 1-279 <WHI>
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A;Experimental source: strain R1
C;Genetics:
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A;Experimental source: strain Bristol N2; clone F10D2
C;Genetics:
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Rigarves, T.; Wohldmann, P.; Gillam, B.
Rigarves, T.; Wohldmann, P.; Gillam, R.
Rigarves, T.; Wohldmann, P.; Gillam, R.
Rigarves, T.; Wohldmann, P.; Wohldmann, R.
Rigarves, T.; Wohldmann, R.
Rigarves, T.;
                                                                                                                  Gaps
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C;Superfamily: Deinococcus radiodurans hypothetical protein DR0271
              65.4%; Score 34; DB 2; Length 126; 66.7%; Pred. No. 8.2; vative 1; Mismatches 2; Indels
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Pred. No. 19;
0; Mismatches 2; Indels
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A;Introns: 37/2; 90/1; 113/1; 183/3; 356/3; 380/3; 428/2
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         Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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218 ENIVPTGKHH 227
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RESULT 10 A69284

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C;Superfamily: AIDS trans-regulatory splicing protein C;Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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N.Alternate names: anti-repression trans-activator; art protein; rev protein; trs protein
C;Species: simian immunodeficiency virus SIVCpz
A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S09988
R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Asture 345, 356-359, 1990
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: S09983; MUD:90259077; PMID:2188136
                                                                                                                                                                                                                                                                             A/Status: preliminary
A/Molecule type: DNA
A/Molecule type
A/Mole
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A;Molecule type: DNA
A;Residues: 1-46 «KUR»
A;Cross-references: GB:AE007317; PIDN:AAK99713.1; PID:g15458516; GSPDB:GN00174
                                                                                       A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Aference number: A89758; MUID:21311952; PMID:11418146 A; Accession: P89892
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     Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, et 357, 1225-1240, 2001
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62.5%; Pred. No. 4.5;
ive 1; Mismatches 2; Indels
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Pred. No. 82;
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Best Local Similarity 62.5
Matches 5; Conservative
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A;Gene: rev; trs; art
A;Introns: 27/1
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A; Residues preliminary
A; Molecule type: DNA
A; Residues 1.156 cSIN-
A; Residues 1.156 cSIN-
A; Residues 1.156 cSIN-
A; Cross = references: GEB-AE004014; GB:AE003849; NID:g9107044; PIDN:AAF84752.1; GSPDB:GNO
A; Experimental source: strain 9a5c
R; Simpson, A.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as-Neco, B.; Docena, C.; El-Dorry, H.; Pacincani, A.P.; Perreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Perreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fro
J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramec, E.F.; Lai
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
A; Mathores: Matins, E.M.F.; Madeiwa, A.Y.; Manck, C.P.M.; Miracca, E.C.; Myaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.Rodrigues, V.; Rosa, A.J. de M.; de Silva, A.C.; de Silva, M.; Silva Jr., W.A.; da Silva
A; Atthores: da Silva, A.C.R.; Perro, da Silva, A.M.; Silva Jr., W.A.; da Silva
A; Reference nunber: A59328
A; Contentes annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: D82618
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence 406, 151-157, 2000
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Feference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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Length 124
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Score 33; DB 1;
Pred. No. 13;
1; Mismatches
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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 22, 2003, 16:43:51 ; Search time 4.6 Seconds

(without alignments)

112.455 Million cell updates/sec
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Title: US-09-909-164-42
Perfect score: 52
Sequence: 1 EEVVPXGXHYS 11
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	O870x9 vibrio para	Q8rg86 fusobacteri	P13390 bacteriopha	P31619 tobacco yel								O26806 methanobact					-	_		Q62190 mus musculu	P97885 rattus norv				ģ	4			-	P44677 haemophilus	•	8	P34335 caenorhabdi
	10	AROA VIBPA	CARB_FUSIN	VLTF_BPTS	Y11K_TYDVA	TKNK BOVIN	CARB_STAAM	CARB STAAW	REV SIVCZ	UMBI_YEAST	MDLB_BUCBP	YK47_YEAST	GAAB_METTH	ALFB_SHEEP	SUOX_DROME	MUTL_BACSU	ETR1_BRAOL	BTR1_ARATH	CENC_MOUSE	YQS6_CAEEL	RON MOUSE	SZOS RAT	MSRA VIBCH	YHA1 CRYPA	ALFB_HUMAN	ALFB_RABIT	THIK ECO57	THIK_ECOLI	THIK_SALTY	SLS1_YARLI	TOLB HAEIN	YL15_VIBPA	DHP1_SCHPO	KPBA_CAEEL
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. مد	당선	69.2	~	67.3	65.4	65.4	65.4	65.4	ω.	ë.	•	•		•	61.5			•		61.5			9,69	59.6	59.6	59.6	59.6	•		e,	59.6	٠.	59.6	59.6
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R PRINTS; PRO0186; CPSASE.
)R TIGRPAMS; TIGRO1369; CPSASE.
)R TIGRPAMS; TIGRO1369; CPSASE.
)R PROSITE; PS00866; CPSASE.
DR PROSITE; PS00866; CPSASE.
DR PROSITE; PS00866; CPSASE.
DR ATGINION MANGANESE; Complete protecome.
KW ATGINION MANGANESE; Complete protecome.
FT DOMAIN 1 401 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
402 546 CLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 184:2005-2018(2002).
-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + pobephate + L-glutamate + carbamoyl phosphate.
-!- COFACTOR: Binds 3 manganese ions per subunit (By similarity).
-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Optimidine biosynthesis; first step.
-!- COFACTOR of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Bhattacharyya A., Batrman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Ponstein M., Xyrpidas N., Overbeek R.;
Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";
                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphare synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphare synthetase ammonia chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANIESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                 Fusobacterium nucleatum (subsp. nucleatum).
Bacteria, Fusobacteria, Fusobacterales, Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE010554; AAL94625.1; ALT_INIT.
HAWAP; MF 01210; -; 1.
InterPro; IPR006275; Cara L glu.
InterPro; IPR005483; CPase L.
InterPro; IPR005409; CPase L. D2.
InterPro; IPR005409; CPase L. D3.
InterPro; IPR005401; CPase L. D3.
InterPro; IPR005401; CPase L. D3.
InterPro; IPR005401; CPase L. D3.
InterPro; IPR004362; MGS 11Ke.
Pfam; PP00219; CPSase L. Chain; 2.
Pfam; PP02786; CPSase L. Chain; 2.
Pfam; PP02786; CPSase L. D3; 1.
Pfam; PP02142; MGS; 1.
                                                   STANDARD;
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546
1058
210
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                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=76856;
                                                                                                                                                                                                                             CARB OR FN0422.
                                                   CARB FUSIN
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NP BIND
NP BIND
METAL
METAL
                       CARB FUSIN
     RESULT 2
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                                                                                                                                                                                   Gape
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Vicuses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
T5-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between early and late genes.";
Nucleic Acids Res. 16:6230-6230(1988).
-1- FUNCTION: NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Kaliman A.V., Kryukov V.M., Bayev A.A.;
"The nucleotide sequence of bacteriophage T5 DNA at the region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95309401; PubMed=7789514;
Kaliman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.,
Kryukov V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The nucleotide sequence of the bacteriophage T5 ltf gene."; FEBS Lett. 366:46-48(1995).
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                                                                                                                        Score 35; DB 1; Length 1058;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                986 986 V -> A (IN REF. 2).
1396 AA; 147989 MW; 18CD2192P65FFFC1 CRC64;
MANGANESE 2 (BY SIMILARITY)
MANGANESE 3 (BY SIMILARITY)
MANGANESE 3 (BY SIMILARITY)
MW; ED7037AF77C1839F CRC64;
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaliman A.V.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                     VLTF_BPT5

1D VLTP_BPT5

1D VLTP_BPT5

1D VLTP_BPT5

1D VLTP_BPT5

10.-JAN-1990 (Rel. 13, Created)

1D 10.-FRB-1996 (Rel. 33, Last sequence update)

1D 10.-MAY-2000 (Rel. 39, Last annotation update)

1D 10.-MAY-2000 (Rel. 39, Last annotation update)

10.-Bhaped tail fiber protein (LTF protein).
                                                                                                                                                                                 2; Mismatches
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PIR; S65934; S36851.
Late protein.
CONFLICT 986 986 V
SEQUENCE 1396 AA; 147989 MW;
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. 300 300
820 820
832 832
1058 AA; 117451 M
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Best Local Similarity 50.vv.
Best Local Similarity 50.vv.
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190 BIVPNGLNYS 199
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Best Local Similarity
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Buropean Bioinformatics Institute.
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ID CARB STAAM
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SEQUENCE
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-!- FUNCTION: TACHYKININS ARE ACTIVE PRETIDES WHICH EXCITE NEURONS, EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SWOOTH
                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=92188538; PubMed=1546458;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
The nucleotide sequence of the infectious cloned DNA component of
tobacco yellow dwarf virus reveals features of geminiviruses
infecting monocotyledonous plants.";
Virology 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.4%; Score 34; DB 1; Length 102; 60.0%; Pred. No. 3.2; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002621; Gemini mov.
Pfam. PF01708; Gemini mov; I.
Hypothetical protein. SEQUENCE 102 AA; 11178 MW; AAOECFIEOAF55B67 CRC64;
                                                                                                     Tobacco yellow dwarf virus (strain Australia) (TVDV)
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted. SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurokinin B precursor (NKB) (Neuromedin K)
TAC3 OR NKNB.
                                                  Last sequence update)
Last annotation update)
           102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 AA
                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-CCT-1993 (Rel. 27, Last anno
Hypothetical 11.2 kDa protein.
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01-NOV-1988 (Rel. 09, Last seq
                                                                                                                                                                                                                                                                                                                                                                              EMBL; M81103; AAA47947.1; -.
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            STANDARD:
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7 QVVPSGINYS 16
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                                                                                                                              NCBI_TaxID=31599;
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P08858;
           Y11K TYDVA
P31619;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.

-1- COPACTOR: Binds 3 manganese ions per subunit (By similarity).
-1- PATHWAY: Arginine biosynthesis.
-1- PATHWAY: Pytimidine biosynthesis; first step.
-1- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
There are no restrictions on
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STRAIN-MISO, ARCC 700699, and N315;
MEDLINE-21311952; PubMed=11418146;
MEDLINE-21311952; PubMed=11418146;
MIDLINE-21311952; PubMed=11418146;
MIDLINE-21311952; PubMed=11418146;
MIDLINE-21311952; PubMed=11418146;
MIDLINE-21311952; PubMed=11418146;
MIDLINE-21311952; PubMed=11418146;
MIDLINE-21311952; MIDLINE-2131196;
MIDLINE-21311952; MIDLINE-2131196;
MIDLINE-21311952; MIDLINE-2131196;
MIDLINE-2
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (BC 6.3.5.5) (Carbamoyl-phosphate synthetase amonia chain).
CARB OR PYRAB OR SAV1203 OR SA1046.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain Mu55).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                   R RWEL; M14347; AAA30723.1; JOINED.

R RWEL; M14348; AAA30723.1; JOINED.

R RWEL; M14349; AAA30723.1; JOINED.

R RWEL; M14350; AAA30723.1; JOINED.

R DIR; A25905; A25905.

R InterPro; IPR003635; Neurokinin.

R InterPro; IPR002040; Tachykinin.

R Pfam; PF00393; Neurokinin B; 1.

R ProDom; PD020370; Neurokinin B; 1.

R PROSITE; PS00267; TACHYKININ; 1.

R Tachykinin; Neuropeptide; Cleavage on pair of basic residues; Amidation; Signal.
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SIMILARITY: BELONGS TO THE CARB FAMILY.
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86 95 NEC
99 126 AM
126 AA; 13871 MW; 4
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REV SIVCZ
P17280;
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SEQUENCE
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            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the between also informatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                      Refam; Froz. MGS; 1.

R PRINTS; PR00098; CPSASE.

R TIGREAMS; TIGRO1369; CPSASE.

R TIGREAMS; TIGRO1369; CPSASE.

DR PROSITE; PS00866; CPSASE.1; 2.

DR PROSITE; PS00866; CPSASE.2; 2.

KW Arginine biosynthesis; Pytimidine biosynthesis; Ligase; Repeat;

KW Arginine biosynthesis; Complete protecome.

FT DOMAIN

TOMAIN

FT DOMAIN

S47 GARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.

TOMAIN.

TOMAIN.

TOMAIN.

TOMAIN.

TOMAIN.

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MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; FubMed=12044378;
Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yanamoto K., Hiramateu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2004 (Rel. 41, Last annotation update)
28-FEB-2005 (Rel. 41, Last annotation update)
phosphate synthetese ammonia chain (EC 6.3.5.5) (Carbamoyl-CARB OR PYRAB OR MW1086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 ATP (POTENTIAL).
52 ATP (POTENTIAL).
84 MANGANESE 1 (BY SIMILARITY).
80 MANGANESE 2 (BY SIMILARITY).
80 MANGANESE 2 (BY SIMILARITY).
80 MANGANESE 3 (BY SIMILARITY).
81 MANGANESE 3 (BY SIMILARITY).
82 MANGANESE 3 (BY SIMILARITY).
83 MANGANESE 3 (BY SIMILARITY).
84 MANGANESE 3 (BY SIMILARITY).
85 MANGANESE 3 (BY SIMILARITY).
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Pred. No. 36;
1; Mismatches 3; Indels
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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                                                                                                              EWBL; AP003361; BAB57365.1; -...
EWBL; AP003132; BAB42298.1; -...
HSSP; P00968; 1CSO.
HAMAP; MF 01210; -; 1...
InterPro; IPR00545; CarA L glu.
InterPro; IPR005483; CPase L D2.
InterPro; IPR005481; CPase L D2.
InterPro; IPR005481; CPase L D3.
Fram; PP00299; CPSase L Chain; 2.
Fram; PP02788; CPSase L Chain; 2.
Fram; PP02789; CPSase L D3; 1...
Pfam; PP02787; CPSase L D3; 1...
Pfam; PP02142; MGS; 1...
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Matches 6; Conserv
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                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00867; CPSASE 2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat; ATP-binding; Manganese; Complete protecome.

**CARBOXPHOSPHATE SYNTHETIC DOMAIN.**

1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 MANGANESE I (BY SIMILARITY).
98 MANGANESE I AND 2 (BY SIMILARITY).
00 MANGANESE 2 (BY SIMILARITY).
20 MANGANESE 3 (BY SIMILARITY).
312 MANGANESE 3 (BY SIMILARITY).
117185 MW; D8E3B09F9EGF152 (CRC64;
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(Rel. 15, Last sequence update)
(Rel. 41, Last annotation update)
(Anti-repression transactivator protein) (ART/TRS).
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Genome and virulence determinants of high virulence community.
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ATP (POTENTIAL)
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Pred. No. 36;
1; Mismatches
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TIGRAMS; TIGRO1369; CPSASE11_lrg; 1.
PROSITE; PS00866; CPSASE 1; 2.
PROSITE; PS00867; CPSASE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMEL, AP004825; BAB94951.1; -- HAWAP; MF 01210; -; 1
InterPro; IPR005455; CarA L glu.
InterPro; IPR005483; CPase L.
InterPro; IPR005489; CPase L.
InterPro; IPR005489; CPase L.
InterPro; IPR005489; CPase L.
InterPro; IPR005481; CPase L.
Pfam; PP00289; CPSase L. Chain; 2.
Pfam; PP00289; CPSase L. Chain; 2.
Pfam; PP027845; CPSase L. Chain; 2.
Pfam; PP027845; CPSase L. D3; 1.
Pfam; PP021842; MGS; 1.
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01-AUG-1990 (
28-FEB-2003 (
REV protein (
REV.
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MOLB BUCBP
Q89A96;
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MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

A Raujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

A Raujo R., Aparicio A., Barrell B.G., Carpenter J., Cherry J.M.,

A Chung R., Churcher C.M., Coster P., Davis R., Davis R.W.,

A Dietrich F.S. Delius H., Dipaolo T., Dubois B., Duesterhoeft A.,

A Dietrich F.S., Delius H., Dipaolo T., Pritz C., Goffeau A.,

A Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,

A Hanicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,

A Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis B.J.,

Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,

A Marather S., Namath A., Nentwich U., Oefner P., Pearson D.,
                                                       MEDLINE=90259077; PubMed=2188136;
Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                             NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
--- SUBCELULAR LOCATION: NUCLear; accumilates in the nucleoil.
--- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.
                                                                                                                          Nacure 345:356-359(1990).
-i- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation, AIDS; Phosphorylation; Nuclear protein. SEQUENCE 124 AA; 13701 MW; F5877D1BDF65A7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.5%; Score 33; DB 1; Length 124; 60.0%; Pred. No. 6.5; 3; Indels iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mailory M.J., Strich R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11723,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNEI YEAST STANDARD; PRT; 460 AA. 003010; P87330; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) Meiosis negative regulator UMEI. UMEI OR WIM3 OR YPLI39C OR LEITC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000625; REV protein.
Pfam; PF00424; REV; 1.
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Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H., Hani J.; "The mucleotide sequence of Saccharomyces cerevisiae chromosome XVI."; Nature 387:103-105(1997).
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Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,
Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
"Reductive genome evolution in Buchnera aphidicola.";
Proc. Natl. Acad. Sci. U.S.A. 100:881-586(2003).
-1- SUBCELLUMA LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Buchnera.
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                                                                                                                                                                                                  GO; GO:0005644; C:nucleus; IDA.
GO; GO:0003714; F:transcription co-repressor activity; IDA.
GO; GO:000020; P:regulation of meiosis; IGI.
InterPro; IPRO01660; WD40.
SMART; SM00320; WH40; 4.
PROSITE; PS00678; WD REPEATS 1; FALSE NEG.
PROSITE; PS500824; WD REPEATS 2; FALSE NEG.
PROSITE; PS500824; WD REPEATS REGION; FALSE NEG.
TEALSCRIPTORY REGULATION; Meiosis; Repeat; WD repeat.
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Pred. No. 25;
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15-5EP-2003 (Rel. 42, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
Multidary resistance-like ATP-binding protein mdlB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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80 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 IVPLGLHY 92
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POTENTIAL.

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1 REVVPXGXHYS 11
          TRANSMEM
 TRANSMEM
                                                                                                                                                                 RESULT 12
GAAB METTH
                                                                         Matches
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                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buspean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch.
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0004565; F:glycerol-3-phosphate O-acyltransferase acti. . .; IDA.
GO; GO:0008654; P:phospholipid biosynthesis; IDA.
GO; GO:0008654; P:phospholipid biosynthesis; IDA.
InterPro; IRR002123; Acyltransferase.
Pfam; PPO1553; Acyltransferase; 1.
SMART; SM00563; PisC; 1.
Hypothetical protein; Transmembrane.
TRANSMEM 69 85 POTENTIAL.
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
STRAIN=S288C;
van Vliet-Reedijk J.C., Planta R.J.;
Submitted (WaR-1994) to the EMBL/Genbank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: STRONG, TO YEAST YBL011W.
                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 83.6 kDa protein in CCP1-MET1 intergenic region.
YKRO67W.
                                                                                                                                                                                                                                                                                              Score 33; DB 1; Length 578;
Pred. No. 31;
                                                                                                                           PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Transport; Transmembrane; Complete proteome.
TRANSMEM 26 46
POTENTIAL.
                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                       3B84848CE196ADF7 CRC64;
                                                                                                                                                                                                                                            ABC TRANSPORTER. ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                           743 AA.
                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                        66827 MW;
                                                                                                                EMBL; AE014017; AA027134.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z28292; CAA82146.1; -. PIR; S38143; S38143. SGD; S0001775; GPT2.
                                                                                                                                                                                                                                                                                                 63.5%;
                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                             550 EIVESGTHYN 559
                                                                                                                                                                                                                                                                                                                                                    2 EVVPXGXHYS 11
                                                                                                                                                                                                                                                                        578. AA;
                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                           YK47 YEAST
                                                                                                                                                                                                                                            DOMAIN
NP BIND
SEQUENCE
                                                                                                                                                                             TRANSMEM
TRANSMEM
TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                            YK47_YEAST
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WEDLINE-98037514, PubMed=9371463;

WEDLINE-98037514, PubMed=9371463;

MEDLINE-98037514, Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,

Aldredge T., Bashirzadeh R., Bakely D., Cook R., Gilbert K.,

Aldredge T., Bashirzadeh R., Falzely D., Cook R., Gilbert K.,

Marrison D., Hoang L., Keagle P., Lumm W., Pothiser B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

A Jivani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

Anniels C.J., Mao J.-I., Rice P., Noelling J., Reveve J.N.;

"Complete genome sequence of Methanobacterium thermoauctcrophicum

deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 1797135-7155(1997).

J. Bacteriol. 1797135-7155(1997).

C.I. CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine +

H(2)0 = AMP + diphosphate + GMP + L-glutamate.

C.I. PATHWAY: GMP biosynthesis.

C.I. SUMINAY: GMP Diosynthass SUBUNIT (B) (POTENTIAL).

C.I. SUMINARITY: BELONGS TO THE GMP SYNTHASE PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                 Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
GMP synthase [glutamine-hydrolyzing] subunit B (BC 6.3.5.2) (GMP
                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea, Buryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PP00958; GMP synt C; 1.
TIGRPAMs; TIGR00884; guaA Cterm; 1.
Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
                                                                                                             Score 33; DB 1; Length 743;
Pred. No. 41;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%; Score 32; DB 1; Length 308; 63.6%; Pred. No. 27; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 184 GMP-BINDING (BY SIMILARITY).
29 35 ATP (BY SIMILARITY).
308 AA; 34403 MW; P2DCF6ED202CAECI CRC64;
                               POTENTIAL.
84B9946E56B82F15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000850; AAB85215.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MP_00345; -; 1.
InterPro; IPR001674; GMP_synt_C.
                                                              83644 MW;
                                                                                                             63.5%;
                                                                                                                                                  Local Similarity 75.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                     294 VVPCGLHY 301
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Best Local Similarity
Local 7; Conserva
                                                                                                                                                                                                                                          3 VVPXGXHY 10
502 5
539 5
743 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthetase).
GUNAB OR MTH710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAB METTH
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SEQUENCE
                                                                                                                   Query Match
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573 AA.

PRT;

STANDARD;

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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable sulfite oxidase, mitochondrial precursor (RC 1.8.3.1).
                                                                                                      Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                            Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                     MEDLINE-20196006; PubMed=10731132;
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                       STRAIN-Berkeley;
  SUOX DROMB
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                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase).
ALDOB.
                                                                                                                                                                                                                                                                                                                  "Cloning and characterization of a full-length cDNA coding for ovine aldolase B from fetal mesonephros.";
Biochim. Biophys. Acta 1219:223-227(1994).
-!- CATALYTIC ACTIVITY: D-fructose 1, 6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.
-!- PATHWAY: Glycolysis; sixth step.
-!- PATHWAY: Glycolysis; sixth step.
-!- SUBUNIT: Homocetramer (By similarity).
-!- MISCELLANBOUS: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, aldolase A in muscle, aldolase B in liver and aldolase C in brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 146 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
229 229 SCHIFF-BASE WITH DIMYDROXYAGETONE-P.
363 363 ESSENTIAL FOR ENHANCED ACTIVITY OF THE RIZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
363 AA, 39500 MW, PCBB45666821EZBD CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                             Gianquinto L., Pailhoux E.A., Bezard J., Servel N., Kirszenbaum M.,
                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
ammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
MCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to class I fructose-bisphosphate aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.5%; Score 32; DB 1; Length 363; 62.5%; Pred. No. 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lyase; Schiff base; Glycolysis; Multigene family.

INIT MET

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BINDING

55

55

C-1-PHOSPHATE GROUP (
                                                                                363 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P00883; IADO.
InterPro; IPR00741; Aldolase I.
Ffam; PF00274; glycolytic_enzy; 1.
ProDom; P0001128; Aldolase I; 1.
PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
                                                                              PRT;
                                                                                                                                                                                                                                                                   TISSUE=Mesonephros;
MEDLINE=94368863; PubMed=8086469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z29372; CAA82563.1; +. PIR; S47540; S47540.
216 REVVESGLHRS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 62.5
                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EVVPXGXH 9
                                                                                                                                                                         Ovis aries (Sheep).
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.
                                                                              ALFB SHEEP
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ACT_SITE
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Burton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
R. Bardon R.C., Rogers Y.-H.C., Blazef R.G., Change M., Miklos G.L.G.,
R. Ballew R.M., Baul A., An H.-J., Andrews-Frankoch C., Baldwin D.,
Ballew R.M., Baul A., Baxendala J., Bayraktaroglu L., Beasley B.M.,
R. Besoon K.Y. Bence P.V., Barman B.P., Bhandari D., Bolahakov S.,
Burtis R.C., Busam D.A., Buller H., Cadeu B., Center A., Chandra I.,
R. Burtis R.C., Busam D.A., Buller H., Cadeu B., Center A., Chandra I.,
R. Burtis R.C., Busam D.A., Buller H., Cadeu B., Center A., Chandra I.,
R. Burtis R.C., Busam D.A., Buller H., Cadeu B., Center A., Chandra I.,
R. Burtis R.C., Gabrielian A.E., Gorg P. Gorrell J.H., Galser K.,
B. Golder A., Gong F. Gorrell J.H., Guz., Gelbart W.M., Glasser K.,
Alordhu K.J., Kangelista C.C., Ferraz C., Ferriars S., Pleitz S.,
R. Hostin D., Houston K.A., Hawland T.J., Werlandez J.R., Houston D.,
R. Hostin D., Houston K.A., Hawland T.J., Werlander S., Rilp D., iai Z.,
Alali M., Kalush F., Karpen G.H., Ka Z., Kannison J.A., Ketchum K.A.,
Jall M., Malteri B., McIntosh T.C., McLead M.P., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Weisser M.G.,
Ralaner K., Salden-Kiames I., Simpon M., Stupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
Ryinkas R., Tector C., Turner R., Venter E., Wang A.H., Wang K.,
Millams S.M., Woodey T., Weinsenbach J.,
Milliams S.M., Woodey E.W., Weinsenbach J.,
Milliams S.M., Woodey E.W., Weinsenbach J.,
Milliams S.M., Woodey E.W., Rubin G.M., Weissenbach J.,
Milliams S.M., Woodey E.W., Weinsenbach J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAINS-Berkeley; TISSUB-Embryo;

MEDLINE-22456066; PubMed=12537569;

Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,

George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,

Rubin G.M., Celniker S.B.;

"A brosophila full-length CDNA resource.";

Genome Biol. 3:RBSBARCH0080.1-RBSBARCH0080.8(2002).

-I- CATALYTIC ACTIVITY: Sulfite + O(2) + H(2)O = sulfate + H(2)O(2).

-I- COPACTOR: Molybdenum (molybdopterin) and one protoheme group (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Terminal reaction in the oxidative degradation of sulfur-containing amino acids. It uses cytochrome c as an electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Mitochondrial intermembrane space (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: WITH CYTOCHROME B5 AND NITRATE REDUCTASE. SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
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RESULT 14 SUOX\_DROME

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                            ProDom; PD000612; Cyt B5; 1.
PROSITE; PS00191; CYTOCHROME B5 1; 1.
PROSITE; PS0025; CYTOCHROME B5 2; 1.
PROSITE; PS00559; MOLYBDOPTREIN EWK; FALSE NEG.
Hypothetical protein; Oxidoreductase; Mitochondrion; Heme; Molybdenum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
-i- CAUTION: It is not obvious if the molybdenum-pterin domain is functional; the conserved cysteine (position 339) is replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ginetti F., Perego M., Albertini A.M., Galizzi A., "Bacillus subtilis mutS mutL operon: identification, nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLYBDENUM-PTERIN (BY SIMILARITY).
71AB1D2B3465D811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                             GO; GO: 0005758; C: mitochondrial intermembrane space; NAS. GO; GO: 0005758; C: mitochondrial intermembrane space; NAS. GO; GO: 0008482; F: sulfite oxidase activity; NAS. GO; GO: 000163; P: spotein catabolism; NAS. anterpro: PR00163; P: pub. Mb. oxred. Interpro: IPR00159; Cyt. BS. Interpro: IPR005065; Mo-Co_dimer. Interpro: IPR005066; Mo-Co_dimer. PF6an; PP00173; heme 1; 1.

R Ffan; PP00174; Mo-Co_dimer; 1.

R Ffan; PR00174; MO-Co_dimer; 1.

R Ffan; PR00174; MO-Co_dimer; 1.

R FRINTS; PR00363; CYYCCHROMEBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 1; Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLYBDENUM-PTERIN DOWAIN (BY
IRON (HEME AXIAL LIGAND) (BY
IRON (HEME AXIAL LIGAND) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus. NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                        PROBABLE SULFITE OXIDASE. HEME-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                  HINGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             627 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96349107; PubMed=8760914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA mismatch repair protein mutL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and mutagenesis.";
Microbiology 142:2021-2029(1996).
                                                                                                                                    EMBL; AE003510; AAF48894.1; -. EMBL; AY069352; AAL39497.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64346 MW;
                                                                                                                                                                      FlyBase; FBgn0030966; CG7280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| :| | ||
503 QEEMPDGRHY 512
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                                                                                                                                                                                                                                                                                                                                                                                                                 187
207
144
168
168
287
573 AA;
                                                                                                                                                            HSSP; P07850; 1SOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     Transit peptide
TRANSIT
                         Ile-339.
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P49850;
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R. MEDLING-SOUGHAND : Publication 1., Albertini A.M., Alloni G.,
R. Agravedo V., Bensiere M.G., Bessieres P. Bofolth. A., Berchert S.,
R. Agravedo V., Bensiere M.G., Bessieres P. Bofolth. A., Berchert S.,
R. Denisor R., Bensiere M.G., Bessieres P. Bofolth. A., Berchert S.,
R. Denisor R., Bensiere M.G., Choult J., Torneston I.F., Commission I.R.,
R. Berling R., Bensiere M.G., Grant J., Torneston I.F., Commission I.R.,
R. Berling R., Bensiere M.G., Grant S., Gallati A., Gallaten N.,
R. Adlan K.D., Grant J.J., Descention I.F., Endish R.J., Grand G.
R. Adland R. C., Poylate R. M., Polita E. Y., Daneston P. T.,
R. Adland R. C., Poylate R. M., Polita E. Y., Bared S., Gallati A., Gallaten N.,
R. Adland R. C., Poylate R., Polita E., Radiol C., Reinal R. A.,
R. Adland R. C., Poylate R., Polita E., Radiol C., Reinal R. A.,
R. Marie R. W., Faderpol S., Reson S. M., Mallo R. F., Card G.
R. Marie R. M., Faderpol S., Reson S. M., Mallo R. Wallon C., Medigue C.,
R. Mones B. C., Reilly R., Carlado R., Hauld G., Medal G., Medal
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Q884ul streptococc Q84281 streptococc Q845q1 streptococc Q845q1 streptococc Q895y4 streptococc Q81011 plasmoduum Q96yh5 sulfolobus Q86yu7 streptococc Q93xq4 canis famil Q57489 bacteroides Q81013 bos taurus Q81013 bos taurus Q81013 bos taurus Q8yup1 anabaena sp Q89syn1 plasmodium Q85xh1 plasmodium Q95xh1 plasmodium Q95xh1 plasmodium Q95xh1 plasmodium Q95xh1 plasmodium

097qm8 streptococc Q9aht9 streptococc Q9any3 streptococc Q9avk4 pisum sativ

OM protein

Run on:

Sequence:

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Ol-OCT-2002 (TERMELrel. 22, Created)
01-OCT-2002 (TERMELrel. 22, Last sequence update)
01-MAR-2003 (TERMELrel. 23, Last annotation update)
Similar to expressed sequence A1987856.
1110004815RIK.
Mus musculus (Mouse)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strauberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032195; AAH32195.1; -.
MGD; MGI:1915724; 1110004B19Rik.
BEQUENCE 413 AA; 46621 MW; A9BBAIDC70CDA0D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
78.8%; Score 41; DB 11;
Best Local Similarity 63.6%; Pred. No. 2.1;
Matches 7; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                  QBE4U1
QBEZB11
QBEZB12
QBESC1
QBESC1
QBETB11
QBETW1
QBECW1
QBECW1
QBECW1
QBECW1
QBEW1
QBEW
                                      168 RRIPPLGKHYS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Q8K289
Q8K289;
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046486
1D 046
AC 046
DT 011-
DT 011-
DB HYE
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Q46486 corynebacte
Q80794 stephylococ
Q40479 nicotiana t
Q91w50 nicotiana t
Q91x70 methanobact
Q904x6 cercopithec
Q8711 brucella me
Q8711 brucella me
Q8711 brucella me
Q8711 brucella me
Q91x19 dinococcc
Q91xx19 dinococcc
Q91xx19 dinococcc
Q91xx19 dinococcc
Q91xx19 thermoplasm
O16912 caenorhabdi
                                                                                                                              December 22, 2003, 17:27:26; Search time 25.2 Seconds (without alignments) 112.642 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                              830525
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                       830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
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Q46486
Q40479
Q40479
Q9LW50
Q9BHU6
Q9RTD
Q27679
Q9RIX6
Q9RIX6
Q8IX10
Q8DIX10
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sp_archea:*
sp_bacteria:*
sp_human:*
sp_human:*
sp_nammal:*
sp_ncyanelle:*
sp_organelle:*
sp_organe
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Gapop 10.0 , Gapext 0.5
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Sp_bacteriap:*
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seq length: 200000000
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52
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Match Length DB
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Minimum DB Maximum DB

Database

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Gaps

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Q46486 PRELIMINARY; PRT; 208 AA.
Q46486;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NAR-2001 (TrEMBLrel. 16, Last annotation update)
GCRA.

Q9RXN9 Q9HLH8 O16912

Result Š

Length 413; 3; Indels

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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, lamiids; Solanales; Solanaceae, Nicotiana.
                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-BY4; TISSUB=Leaf;

A MEDLINEs-S276469; bubmed=7756828;

A Obme-Takagi M., Shinshi H.;

Thylene-inducible DNA binding proteins that interact with an ethylene responsive element.";

Thylene responsive element.";

Plant Cell 7:173-182(1995).

REMBL; D38126; BAA07324.1; -..

REMBL; D38126; BAA07324.1; -..

REMBL; D38126; BAA07324.1; -..

REMBL; D38126; BAA07324.1; -..

REMBL; D88126; BAA07321.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana sylvestris (Wood tobacco).
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, lamiids; Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 35; DB 10; Length 233; 60.0%; Pred. No. 23; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 AA; 26243 MW; 01BC3EEB51E46298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) 8thylene-responsive element binding factor.
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.3%; Score 35; DB 10;
60.0%; Pred. No. 23;
ive 1; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 AA
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                                                           KREBP-2.
Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 AA; 25563 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 QAVVPKGRHY 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4096;
                                                                                                                                                       NCBI_TaxID=4097;
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                                                                                                                                                                                                                                                                                                                  SPECIES=C.striatum; STRAIN=M82B;
MEDLINE=20194806; PubMed=1073568;
Tauch A., Krieft S., Kalinowski J., Puhler A.;
"The 51,409-bp R-plasmid pTP10 from the multiresistant clinical isolate Corynebacterium striatum M82B is composed of DNA segments initially identified in soil bacteria and in plant, animal, and human pathogens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                       SPECIES=C.xerosis; STRAIN=M82B; MEDIATE=6517603; PubMed=6559800; Tauch A., Kassing F., Kalinowski J., Puhler A.; Tauch A. Kassing F., Kalinowski J., Puhler A.; Truch A. Corynebacterium xerosis composite transposon Tn5432 consists of two identical insertion sequences, designated IS1249, flanking the erythromycin resistance gene ermCX."; plasmid 34:119-131(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oin Z.,
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NCBI_TaxID=1725, 43770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2; Length 208;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang Y., Ren S., Li H., Pu G., Lu L., Lu G., Jia J., Tu
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AR016746; AR01646.1; -. Complete protect 117391 MW; 8944D7D8DB1CAES9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Gen. Genet. 263:1-11(2000).

EMBL; U21300; AAC95478.1; -.

EMBL; AF024666; AAG03300.1; -.

Hypothetical protein; Plasmid.

SEQUENCE 208 AA; 23012 MW; P1504BEIECDE85A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1057 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carbamoyl-phosphate synthase large chain
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50.0%;
        Corynebacterium xerosis, and Corynebacterium striatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 KEVVSNGLHYS 199
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130 DVIPEGKHYA 139
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Best Local Similarity
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STRAIN=ATCC 12228;
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Matches

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RESULT 3

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Gaps

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233 AA

PRT;

PRELIMINARY;

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RESULT 4

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040419

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PRINTS; PR00721; STOMATIN.
SWART; SM0244; PHB; 1.
Procease; Complete proteome.
SEQUENCE 308 AA; 34778 WW; ADE03603E5101A9D CRC64;
                                                                                                                                                                                                                                                                                       3 VVPXGXHY 10
                                                                                                                                                                                                                                                                                                                                               41 WPSGIHY 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=12417;
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01-NOV-1996 (
01-MAR-2003 (
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-BSB8 / DSM 3109;

WEDLINE-99287316; PubMed-10360571;

Melson K.B., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey B.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

A Haft D.H., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Hedelberg J., Sutton G.C., Fleischmann R.D., Eisen J.A., White O.,

A Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

Revidence for lateral gene transfer between Archaea and Bacteria from

RT Genome sequence of Thermotoga maritima.";

Mature 399:323-329(1999).

REMBL, AE001849; AAD36885.1;

TIGR; TM1822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21082930; PubMed=11214968; Kaneko T., Sagamoto S., Kaneko T., Nakamira Y., Sato S., Asamiru B., Kato T., Sagamoto S., Watanabe A., Idesawa R., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesophizobium loci.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                 Rhizobium loti (Megorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Megorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.3%; Score 35; DB 16; Length 285; 55.6%; Pred. No. 28;
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                                                                                                                        01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
FTSH protease activity modulator HFLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 AA
                                                                    285 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 7:331-338 (2000).
EMBL; AP003000; BAB49770.1; -
InterPro; IPR000345; Cytc heme_bind.
InterPro; IPR002326; Cytc heme_bind.
Pfan; PF03167; Cytcchrome_C1; Pfan; PR00603; CYTOCHROMEC1.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                    PRT;
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band 7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                 PRELIMINARY;
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SEQUENCE 285 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=381;
                                                                                                                                                                                                                      Cytochrome c1.
MLL2705.
                                                                                                                           01-OCT-2001
01-OCT-2001
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                                                                                                    098HIU6;
                                                                 90H860
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RESULT 6
Q98HU6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Engel G., Alterman B., Klein J., Henrich B.;
"Structure of a genome region of the Lactobacillus gasseri temperate phage phi adh covering a repressor gene and cognate promoters.";
Gene 210:67-70(1998).
EMBL, AJ131519, CAB52540.1;
InterPro: IPR002053, Glyco-hydro-25.
InterPro: IPR003646; SH3 bac.
Pfam; PF01183; Glyco-hydro-25; 1.
Probom; PD004620; Glyco-hydro-25; 1.
Probom; PD004620; Glyco-hydro-25; 1.
SMART; SM00641; Glyco-25; 1.
                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactobacillus bacteriophage phi adh.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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Henrich B., Binishofer B., Blaesi U.;
"Frihary structure and functional analysis of the lysis genes
Lactobacillus gasearl bacteriophage phi-adh.";
J. Bacteriol. 177:723-732(1995).
  Length 308;
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66.7%; Pred. No. 32;
ive 1; Mismatches 2; Indels
                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Altermann E.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 AA; 34703 MW; 9FF2715EB43561C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
67.3%; Score 35; DB 16; 75.0%; Pred. No. 31;
                                                       0; Mismatches
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Query Match 67.3
Best Local Similarity 75.0
Matches 6; Conservative
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Matches 6; Conservative
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Gene 126:61-66(1993).
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60 VVPMGYHYA 68

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Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum
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GRAY W.L., Startnes H.B., White M.W., Ashburn C.V., Mahalingam R.;
"Complete Sequence of the Simian Varicella Virus Genome.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275348; AAG27217.1;
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                                                                                                                                                               Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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Pred. No. 36;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155 (1997).
REBL: AE000923; AAB86115.1;
RINTERPRO; IPRO05140; eRF1_2.
RINTERPRO; IPRO05141; eRF1_2.
RINTERPRO; IPRO05141; eRF1_3.
RINTERPRO; IPRO040405; PelA.
Refm: PRO3464; eRF1_1: 1.
Refm: PRO3464; eRF1_2: 1.
Refm: PRO3465; eRF1_3: 1.
Refm: RF03465; eRF1_3: 1.
Refm: RF03465; eRF1_3: 1.
Refm: RF03465; eRF1_3: 1.
Refm: RF03465; eRF1_3: 1.
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678 AA; 75850 MW; A17B09B30512FB3C CRC64;
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SEQUENCE 360 AA; 40814 MW; 2A000CB4B3CEF469 CRC64;
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Alphaherpesvirinae; Varicellovirus.
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 75.9 kDa protein.
                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                Methanobacterium thermoautotrophicum.
                                                                Created)
                               PRT;
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                                                                                                                                                                                                                                               STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
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                                                            01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2003 (TrEMBLrel. 23,
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98 EDLVPMGSHHT 108
                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EEVVPXGXHYS 11
                                                                                                                  Cell division protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                  NCBI_TaxID=187420;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q9E1X6;
                                                027679;
                             027679
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Matches
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RESULT 9
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               027679
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REMEDINE-20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.P., Suttern G.G., Wortnan J.R., Yandell M.D., Zhang O., Chen L.X., Baraton G.C., Rogers Y.H., Blazej R.G., Champe M., Pfeitfer B.D., R.A. Adadom R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeitfer B.D., R.A. Brandon R.C., Rabadain A., R. H.J., Andrews-Frankoch C., Baldwin D., R. Ballew R.M., Basus A., Barandale J., Bayzaktaroglu L., Beasley R.M., Ballew R.M., Basus D.Y., Berns P.V., Be
                        Gaps
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Celniker S.B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Bayas C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,
Perriera S., Frise E., Galle R.P., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
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                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                        IndelB
                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                        3,
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  Pred. No. 72;
2; Mismatches
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50.08;
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                        Conservative
                                                                                                                                                                                                                       PRELIMINARY;
                                                                                            147 BRIIPKGTRY 156
                                                                   1 BEVVPXGXHY 10
  Best Local Similarity
Matches 5, Conserv
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01-MAR-2003
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STRAIN=16M / ATCC 23456 / Biotype 1;
STRAIN=16M / ATCC 23456 / Biotype 1;
STRAIN=16M / ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=1175688;
DelVecchio V.G., Kapatral V., Red88;
Ivanova N., Andereon I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman B., Selkov E., Bizer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
                                                                                                                     Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.B., Tupy J.L., Bergman E., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Milburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield B., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.B.; Shubrited (MAR-2000) to the EMBL/GenBank/DDBJ databases.
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler P., Stapleton M., Strong R., Svirakas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 5; Length 855;
Pred. No. 93;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003786; AAN16124.1; -. SEQUENCE 855 AA; 94532 MW; 39BD5A516D6312DB CRC64;
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Last annotation update)
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EMBL; AB009470; AAL51457.1; -
InterPro; IPR001086; Aldehyde_dehydr.
InterPro; IPR001410; DEAD.
InterPro; IPR00150; Hellcase_C.
SMART; SM00490; HELICase_C, 1.
SMART; SM00490; HELICC; 1.
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657 DEVVPSGDH 665
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SEQUENCE 1028 A
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Pred. No. 1.2e+02;
1; Mismatches 3; Indels (
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Science 286:1571-1577(1999).
EMBL; AR01889; ARF09867.1; -.
 Score 35; DB 16; Length 1028;
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WCBI_TaxID=1299;
                                      3; Indels
                                                                                                                                                                                                                                                                                                                                   Synechococcus elongatus (Thermosynechococcus elongatus). Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1044 AA; 113205 MW; 00E9C13F0F636D2F CRC64;
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Last annotation update)
                 Pred. No. 1.1e+02;
2; Mismatches 3
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MEDLINE=22225144; PubMed=12240834;
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(TrEMBLrel. 13, I
(TrEMBLrel. 20, I
   67.3%;
54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.6.
Best Local 7, Conservative
                                        6; Conservative
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                                                                         1 EEVVPXGXHYS 11
                                                                                                  |::|| | ||
76 EKIVPPGARYS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 9:123-130(2002)
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Query Match
Best Local Similarity
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01-MAR-2002
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Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 2; Indels
                                       Query Match 65.4%; Score 34; DB 16; Length 279; Best Local Similarity 75.0%; Pred. No. 46; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                        Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
TIGR; DR0271; -. Hypothetical protein; Complete proteome. SEQUENCE 279 AA; 31140 MW; DCEA100E0AEE8831 CRC64;
                                                                                                                                                           09HilB;
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Glucose-fructose oxidoreductase related protein.
                                                                                                                                                     322 AA
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Search completed: December 22, 2003, 17:51:31 Job time : 26.2667 sec8

66 WPDGLHY 73

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Hepatitis C virus

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result No.

Searched:

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/note= "Norvalyl carbonyl forming keto-amide linkage with
    residue 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
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/note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB80544 standard; peptide; 11 AA.
 19-JUL-2001; 2001WO-US23169
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  WO200208251-A2
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Modified-site
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  ABB80544;
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ABB80544
 Hepatitis C virus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                         December 22, 2003, 16:41:00 ; Search time 32.4667 Seconds (without alignments) 53.778 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1981.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                     - protein search, using sw model
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ABB80522
ABB80522
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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48
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Hepatitis C virus Hepatitis C virus Hepatitis C virus

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Local Similarity
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 virus protease
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                                      Brunck TK;
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 (CORV-) CORVAS INT INC
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Pred. No. 0.011
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Claim 17; Page 65; 69pp; English.
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    residue 7"
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                                                                                                                                                                          "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
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                                                                                     Hepatitis C virus, HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
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                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
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                                                                                                                                                          'note= "N-terminal acetyl"
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/note= "C-terminal amide"
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                        ABB80521 standard; peptide; 11 AA.
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Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
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Ity useful for treating disorders associated with hepatitis C
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19-JUL-2001; 2001WO-US23169
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                                                                                                                          Levy OE,
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                     virus protease
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residue 7"
                  /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"
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 /note= "N-terminal acetyl"
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                                      Misc-difference
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Matches
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/note= "Norvalyl carbonyl forming keto-amide linkage with
    residue 7"
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Pred. No. 0.018;
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/note= "C-terminal amide"
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoomide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A
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residue 7"
                                                 The sequence represents a peptide compound of the invention having the peptides of the protesses inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protesses. A pharmaccutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
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Pred. No. 0.018;
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                   Claim 17; Page 64; 69pp; English.
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90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB80536;
                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
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                                                                                                                                                                                                                                     The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus, HCV, serine protease, inhibitor, alpha-ketoamide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
                                                                                                                             Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 23; Length 11;
Pred. No. 0.018;
0; Mismatches 1; Indels
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/note= "C-terminal amide"
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                                                        Brunck TK;
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                                                                                                                                                                                                          Claim 17; Page 64; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                   91.7%;
90.9%;
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                                                        Levy OB,
                   (CORV-) CORVAS INT INC
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                                                                                              WPI; 2002-361643/39
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                                                                                                                                                                        virus protease -
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RESULT 11 ABB80535

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Modified-site
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                                                                                                                                                                                       Synthetic
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Best Local S:
Matches 10
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                                                                                                                                                                                                                                                                                                                             /note= "Norvaly1 carbony1 forming keto-amide linkage with residue 7"
pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                  Gaps
                                                                                                                                                                                                                                  Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
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                                                                                                                                                                                                                    Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #19
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                                                DB 23; Length 11;
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                                               Score 44; DB 23;
Pred. No. 0.018;
0; Mismatches
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                                                                                                                                                         ABB80539 standard; peptide; 11
                                              91.7%;
90.9%;
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                                                                                                                                                                                                (first entry)
                                           Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                      1 BEVVPXGXSYS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                                Misc-difference 8
                            11 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide compound having hepatitis 'C virus protease inhibitory activity useful for treating disorders associated with hepatitis C
                                                                                                                                                                                                                                                                     Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #20
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Pred. No. 0.018;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-terminal acetyl"
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                                                                                                                       ABB80540 standard; peptide; 11
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The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
                                                                                                                                                                                                                                 /note= "Norvalyl carbonyl forming keto-amide linkage with residue ?"
                                                                                               Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
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                                                                              Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #39.
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ABB80559 standard; peptide; 11 AA.
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                                                    08-OCT-2002 (first entry)
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Matches 10; Conservative
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Search completed: December 22, 2003, 17:41:02 Job time : 32.4667 sec8

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MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-637-7598-236
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Sequence 4, Appli
Sequence 26, Appli
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Sequence 27, Appli
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                                                                                                                      December 22, 2003, 16:37:03; Search time 10.1333 Seconds (without alignments) 45.930 Million cell updates/sec
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(c) 1993 - 2003 Compugen Ltd.
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US-08-211-55A-236
US-09-221-945-236
US-09-221-945-236
US-09-221-946-3
US-09-018-211-4
PCT-US91-02714-26
US-09-018-211-4
PCT-US91-02714-2
US-09-46-2
US-08-459-065-2
US-08-459-065-2
US-08-474-379C-28
US-08-474-379C-28
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US-08-474-379C-28
US-08-474-379C-28
US-08-474-379C-28
US-08-915-066-85
US-09-152-066-85
US-09-152-066-85
US-09-152-066-85
US-09-152-066-85
US-09-152-066-85
US-09-152-066-85
US-09-152-066-85
US-09-152-066-85
US-09-152-066-85
US-09-153-084-220
US-08-941-318-319
US-09-941-318-319
US-09-361-083-220
US-09-361-083-220
US-09-361-083-220
US-09-361-083-220
US-09-361-083-220
US-09-361-083-220
US-09-361-083-220
US-09-361-083-280
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                     328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0 seq length: 2000000000
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48
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                                                                                                                                                                                                                           Perfect score:
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Maximum DB
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No.
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US-08-361-517-19
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US-08-440-061-53
US-07-971-096-8
US-08-175-096-8
US-09-047-125-27
US-09-047-125-27
US-08-413-974-4
US-08-413-974-4
US-08-413-978-4
US-08-413-288-4
US-08-413-288-4
US-08-413-288-4
US-08-413-288-6
US-08-413-288-6
US-08-413-974-6
US-08-413-974-6
US-08-413-974-6
US-08-413-974-6
US-08-413-974-6
US-08-413-974-6
US-08-413-288-6
US-08-1175-096-4
US-08-413-974-6
US-08-413-974-6
US-08-413-288-6
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## ALIGNMENTS

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
CLASSIFICATION NUMBER: PCT/GB95/02875
FLING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: PCT/GB95/02875
FLING DATE: 11-DEC-1995
CLASSIFICATION: 435
FLING DATE: 11-DEC-1995
CLASSIFICATION NUMBER: RPMS 101
TREEPHONE: GARACTERISTICS:
TELEPHONE: (404) 873-8795
INPORMATION FOR SEQ ID NO: 236:
SEQUIRNER GARACTERISTICS:
COMPUTER FLOPPERISTICS:
COMPUTER FLOPPERISTICS:
COMPUTER FROM THE FL
Sequence 236, Application US/08637759B
Fatent No. 5876331
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 amino acida
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STRANDEDNESS: single
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Gaps

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Indels

DB 2; Length 45;

Score 32; DB 2; Pred. No. 8.3; 1; Mismatches

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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FRSTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 32; DB 4; Length 45; 60.0%; Pred. No. 8.3; tive 1; Mismatches 3; Indels
                                  ZIP: 30309-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30

CURRAT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                       RPMS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-228-986-73, Application US/09228986; Patent No. 6359198; GENERAL INFORMATION:
                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PADSE, PATERA L.
REGISTRATION NUMBER: 31,284
REPERRENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 BEVVPXGXSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               686 VMPSGISYS 694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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Georgia
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US-08-844-086-4
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Pred. No. 8.3;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: REALABLE FOUR SISTEMS
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
CONTUMER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-UN-1997
CLASSIFICATION 435
PRIOR APPLICATION HAR:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Pablet, Patrea L.
REGISTRATION NUMBER: RPMS 101 CON
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION SEQ 1D NO: 236:
SEQUENCE CHARACTERISTICS:
CROMMUTICATION AS TICS:
CROMMATION FOR SEQ 1D NO: 236:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-201-945-236
sequence 236, Application US/09201945
sequence 236, Application US/09201945
sequence 236, Application US/09201945
sequence 236, Application Of Genes
TOTLE OF INVENTION:
TOTLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Parrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
CONWITE: USA
ZIP: 30199-3450
CONWITER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                              US-08-871-355A-236
; Sequence 236, Application US/08871355A;
; Patent No. 6015669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | : | | | |
1 EEISPLGWSY 10
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ERISPLGWSY 10
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EEVVPXGXSY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Atlanta
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Sequence 26, Application PC/TUS9102714

GENERAL INFORMATION:

APPLICANT: Wichell, John J.

TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSER: Marshall, O'Toole, Gerstein, Murray &

ADDRESSER: Michell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
64.6%; Score 31; DB 3; Length 159;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: STEECT
CITY: CLICAGO
STATE: 111inois
COMPUTER: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPY disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUFTWARE: 19910419
FILING DATE: 19910419
FLING APPLICATION NUMBER: PCT/US91/02714
FILING DATE: 19910419
CLASSIPICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INPORMATION:
NAMME: BOTUN, Michael F.
REGISTRATION NUMBER: 25447
REGISTRATION NUMBER: 25447
TELECOMMUNICATION NUMBER: 27805/30197
TISHECOMMUNICATION NUMBER: 27805/30197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two First National Plaza, 20 South Clark STREET: Street
                                CLASSIPCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,086
FILING DATE: 18-APR-1997
APPLICATION NUMBER: 9607993.4
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: 01mmi, Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 EEVLPDGTS 131
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Pred. No. 53;
1; Mismatches 2; Indels
Sequence 4, Application US/08844086
Patent No. 5866390
GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5866390el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: 709 Swedeland Road
CITY: King of Prussia
STREET: 709 Swedeland Road
CITY: Ring of Prussia
STREET: PA
                                                                                                                                                                                                                                                                                 COUNTY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
APPLICATION NUMBER: USO 1993.4
FILING DATE: 18-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31457-4
TELEPHONE: G10-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09018211
Patent No. 6048716
GENERAL INPORMATION:
AND SEQUENCES:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKiine Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: TEM Compatible
COMPUTER: FastSER for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 64.6%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 159 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-844-086-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 EEVLPDGTS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 REVVPXGXS 9
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US-09-018-211-4
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31 REVVPAG 37
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                                   US-08-459-065-2
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Patent No. 5866405

GENERAL INFORMATION:
APPLICANT: Choi, Gil Ho
APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION Genetically Engineered Transmissible
TITLE OF INVENTION GENETICALION DATA:
STREET: 340 Kingsland Street
CITY: Nutley
STREET: Nutley
STRE
                                                                                                                                                                                                  Score 31; DB 5; Length 513;
Pred. No. 1.9e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 2; Length 622;
Pred. No. 2.4e+02;
0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Endothia parasitica (Cryphonectria ORGANISM: parasitica)
STRAIN: EP713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: ROBEMEN, CALHETINE R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8589
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
TELEFAR: (201) 235-5500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.6%;
85.7%;
                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 622 amino acids
amino acid
LENGTH: 513 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                            201 WPAGGSY 208
                                                                                                                                                                                                                                                                                                                                         3 VVPXGXSY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 EEVVPAG 37
                                                                                                                                   PCT-US91-02714-26
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Paceurine 2, Application US/0045505

Paceurine 2, Application US/0045505

Parent. INCOMMATION:
PAPLICANT: Choi, Gil Ho
APPLICANT: Choi, Gil Ho
APPLICANT: Choi, Gil Ho
APPLICANT: Choi, Gil Ho
APPLICANT: AD KINSTICUS:
MUSSTICUS:
MUSS
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Gaps

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WESULT 12
US-09-146-249A-28
Sequence 28, Application US/09146249A
Sequence 28, Application US/09146249A
Sequence 28, Application US/09146249A
Sequence 28, Application
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Wigler, Michael H.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: 8
STATE: 1110016
CORRESPONDENCE ADDRESS: 8
STATE: 11110016
COMPUTER: Illinois
COUNTY: Chicael Very 233 South Wacker Drive
CITY: Chicael Read States of America
CITY: Chicael Read States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 2; Length 688;
Pred. No. 2.7e+02;
0; Mismatches 2; Indels
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/688,352

FILING DATE: 19-AR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 27866/32771
TELECOMMUNICATION INFORMATION:
TELEFHONE: (312) 474-646
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acide
TYPE: Infortein
US-08-474-379C-28
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTATION NUMBER: 36,107
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRLEX: 25-3856
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-09-146-249A-28
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Best Local Similarity
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US-08-474-379C-28

# KESULT 11
US-08-474-379C-28

# Sequence 28, Application US/08474379C
# Patent No. 5977305

GENERAL INFORMATION:
# APPLICANT: Wigler, Michael H.
# APPLICANT: Wigler, Michael H.
# APPLICANT: CLONING BY COMPLEMENTATION AND RELATED
# TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
# TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
# TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
# TITLE OF INVENTION: 488

# CORRESPONDENCES: 88

# CORRESPONDENCES: 88

# CONFINENCES: 88

# CONFINENCES: 88

# COUNTRY: United States of America
# STATE: Illinois
# COUNTRY: United States of America
# STATE: Illinois
# COUNTRY: United States of America
# COUNTRY: United States of America
# COMPUTER: IBA PC COMPATION:
# MEDIUM TYPE: Ploppy disk
# COMPUTER: IBA PC COMPATION DATA:
# APPLICATION NUMBER: US/08/474,379C
# FILING DATE: US/08/474,379C
# FILING DATE: US/08/474,379C
# PLING DATE: US/08/474,379C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 688;
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                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUGTWARE: Patentin Release #1.0, Version #1.25
SUGTRAREN: Patentin Release #1.0, Version #1.25
SUGTRAREN: Patentin Release #1.0, Version #1.25
SUGNERATION NUMBER: US/07/688,352C
FILING DATE: 19910419
CLASSIPICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
FREGISTRATION NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERPIONE: (312) 346-5750
TELERPIONE: (312) 346-5750
TELERPIONE: (312) 346-5760
TELERRY: 25-3856
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11near
MOLECULE TYPE: protein
US-07-688-352C-28
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